

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:24:31 ; Search time 138.696 Seconds
(without alignments)
81.226 Million cell updates/sec

Title: US-09-462-909D-9
Perfect score: 59
Sequence: 1 XXXXXWSXXXCXGXXXXXX 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03.4
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	69.5	504	2 Q69HL7	Q69hl7 ciona intes
2	41	69.5	3869	2 Q86PQ3	Q86pq3 cryptospori
3	40	67.8	59	2 Q7KY3	Q7ky3 homo sapien
4	40	67.8	238	2 Q76S10	Q76s10 cryptospori
5	40	67.8	238	2 Q69HT6	Q69ht6 ciona intes
6	40	67.8	257	2 Q966K7	Q966k7 caenorhabdi
7	40	67.8	478	2 Q8BVE5	Q8bve5 m mus muscu
8	40	67.8	632	2 Q6ZPQ8	Q6zpq8 mus musculu
9	40	67.8	872	2 Q22580	Q22580 caenorhabdi
10	40	67.8	1077	1 SM5A MOUSE	Q62217 mus musculu
11	40	67.8	1088	2 Q6PCX8	Q6pcx8 xenopus lae
12	40	67.8	1092	2 Q6UY12	Q6uy12 homo sapien
13	40	67.8	1093	1 SM5B HUMAN	Q9p283 homo sapien
14	40	67.8	1093	1 SM5B MOUSE	Q60519 mus musculu
15	40	67.8	1093	2 Q7QC32	Q7qc32 anopheles g
16	40	67.8	1107	2 Q8BHP3	Q8bhp3 mus musculu
17	40	67.8	1122	2 Q7TT33	Q7tt33 mus musculu
18	40	67.8	1151	2 Q6DD89	Q6dd89 homo sapien
19	40	67.8	1170	1 TSPI HUMAN	P07996 homo sapien
20	40	67.8	1170	1 TSPI MOUSE	P35441 mus musculu
21	40	67.8	1170	2 Q715A3	Q715a3 rattus norv
22	40	67.8	1171	2 Q80YQ1	Q80yq1 mus musculu
23	40	67.8	1171	2 Q8CGB2	Q8cgb2 mus musculu
24	40	67.8	1536	2 Q9C014	Q9c014 homo sapien
25	40	67.8	1607	2 Q6P4U0	Q6p4u0 mus musculu
26	40	67.8	1998	2 Q8CG65	Q8cg65 mus musculu
27	40	67.8	5141	2 Q700K0	Q700k0 rattus norv
28	39	66.1	106	2 Q43982	Q43982 cryptospori
29	39	66.1	156	2 Q8MXK6	Q8mxk6 cryptospori
30	39	66.1	168	2 Q9GZ21	Q9gz21 cryptospori
31	39	66.1	168	2 Q9GZ22	Q9gz22 cryptospori

32	39	66.1	168	2 Q9GZ23	Q9gz23 cryptospori
33	39	66.1	192	2 Q7JN23	Q7jn23 cryptospori
34	39	66.1	206	2 Q24927	Q24927 eimeria ten
35	39	66.1	449	2 Q8QFV1	Q8qfv1 xenopus lae
36	39	66.1	461	2 Q9S522	Q9s522 drosophila
37	39	66.1	549	2 Q8T988	Q8t988 drosophila
38	39	66.1	592	1 TOH2_CABEL	P98060 caenorhabdi
39	39	66.1	598	2 Q02029	O02029 drosophila
40	39	66.1	601	2 Q9V746	Q9v746 drosophila
41	39	66.1	612	2 Q6ZQ96	Q6zq96 mus musculu
42	39	66.1	628	2 Q7KRF4	Q7krf4 drosophila
43	39	66.1	654	2 Q19284	Q19284 caenorhabdi
44	39	66.1	656	2 Q86PQ8	Q86pq8 cryptospori
45	39	66.1	660	2 Q23832	Q23832 cryptospori

ALIGNMENTS

RESULT 1
Q69HL7 PRELIMINARY; PRT; 504 AA.
AC Q69HL7;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DE HRTT-1-like (Fragment).
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=23047825; PubMed=14686582;
RA Terajima D., Yamada S., Uchino R., Ikawa S., Ikeda M., Shida K.,
RA Arai Y., Wang H.G., Satoh N., Satake M.;
RT Identification and sequence of seventy-nine new transcripts expressed
RT in hemocytes of Ciona intestinalis, three of which may be involved in
RT characteristic cell-cell communication.";
RL DNA Res. 10:203-212(2003).
DR EMBL; AY261898; AAP91764.1; .
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR001283; Allrgn_V5/Tp1.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000884; TSPI_
DR InterPro; IPR002413; V5_allergen.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR PRINTS; PR00838; V5ALLERGEN.
DR ProDom; PD000542; Allrgn_V5/Tp1; 1.
DR SMART; SM00198; SCP; 1.
DR SMART; SM00209; TSPI; 4.
DR PROSITE; PS01009; CRISP_1; 1.
DR PROSITE; PS01010; CRISP_2; UNKNOWN_1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS50092; TSPI; 5.
FT NON_TER 1
FT NON_TER 504
SQ SEQUENCE 504 AA; 55337 MW; 305F43A92B850F29 CRC64;

Query Match 69.5%; Score 41; DB 2; Length 504;
Best Local Similarity 50.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 WSXXXXCXXCXC 17
Db 477 WSWSACSCTSCG 488

RESULT 2
Q86PQ3 PRELIMINARY; PRT; 3869 AA.
ID Q86PQ3

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AC Q86PQ3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE TSP1 domain-containing protein TSP2 precursor.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22326344; PubMed=12438378;
RX DOI=10.1128/IAI.70.12.6987-6995.2002;
RA Deng M., Templeton T.J., London N.R., Bauer C., Schroeder A.A.,
RA Abrahamson M.S.;
RT "Cryptosporidium parvum genes containing thrombospondin type 1
RT domains."
RL Infect. Immun. 70:6987-6995 (2002).
DR EMBL; AY190984; AAC039046.1; -.
DR HSP; P07996; 1LSL.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR000800; Notch region.
DR InterPro; IPR003582; ShKT.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00066; Notch; 2.
DR Pfam; PF01549; SHTK; 5.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00090; TSP 1; 10.
DR SMART; SM00032; CCF; 2.
DR SMART; SM00004; NL; 6.
DR SMART; SM00254; ShKT; 5.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS00198; 4Fe4S FERREDOXIN; UNKNOWN_3.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00092; TSP1; 10.
KW Signal.
FT SIGNAL.
FT SEQUENCE 3869 AA; 429514 MW; 1F4851B7B0787B87 CRC64;
Query Match 69.5%; Score 41; DB 2; Length 3869;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WSXXXXCSXXCG 17
Db 386 WSSWSCSTSCG 397

RESULT 3
Q7KY3 PRELIMINARY; PRT; 59 AA.
AC Q7KY3; 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Thrombospondin-1p180 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Dimitry J.M., Sheibani N., Finn M., Boak B.M., Paul L.L.,
RX Frazier W.A.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12471; AA21127.1; -.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP1.
DR Pfam; PF00090; TSP_1; 1.

AC PRINTS; PR01705; TSP1REPEAT.
DR PROSITE; PS50092; TSP1; 1.
FT NON_TER 1
FT NON_TER 59
SQ SEQUENCE 59 AA; 6445 MW; C6409E62332708A4 CRC64;
Query Match 67.8%; Score 40; DB 2; Length 59;
Best Local Similarity 50.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WSXXXXCSXXCG 17
Db 22 WSEWTSCTSCG 33

RESULT 4
O76510 PRELIMINARY; PRT; 238 AA.
AC O76510;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thrombospondin-related adhesive protein (Fragment).
GN Name=TRAP-C3;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Moreduin;
RA Spano F., Putignani L., Crisanti A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF073838; AAC26812.1; -.
DR HSP; P07996; 1LSL.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP1; 3.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS50092; TSP1; 3.
FT NON_TER 1
FT NON_TER 238
FT SEQUENCE 238 AA; 26307 MW; 28242DE88F62C5A2 CRC64;
Query Match 67.8%; Score 40; DB 2; Length 238;
Best Local Similarity 50.0%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WSXXXXCSXXCG 17
Db 47 WSSWSCSTSCG 58

RESULT 5
Q69HT6 PRELIMINARY; PRT; 238 AA.
AC Q69HT6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hemocentin-like (Fragment).
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=23047825; PubMed=14686582;
RX Terajima D., Yamada S., Uchino R., Ikawa S., Ikeda K.,
RX Arai Y., Wang H.G., Satoh N., Satake M.;
RT "Identification and sequence of seventy-nine new transcripts expressed
RT in hemocytes of Ciona intestinalis, three of which may be involved in

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RT characteristic cell-cell communication.";

RL DNA Res. 10:203-212(2003).
 DR EMBL; AY261829; AAP91695.1; -.
 DR InterPro; IPR000884; TSP1.
 DR Pfam; PF00090; TSP_1; 4.
 DR SMART; SM00209; TSP1; 4.
 DR PROSITE; PS50092; TSP1; 4.
 FT NON_TER 1
 SQ SEQUENCE 238 AA; 25294 MW; 7C40DAD7D7C57932 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 238;
 Best Local Similarity 50.0%; Pred. No. 5.8;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXXXXXXCG 17
 |||||
 Db 26 WSTFGVCSACG 37

RESULT 6

Q966K7 PRELIMINARY; PRT; 257 AA.
 AC Q966K7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein F14H12.3.
 GN Names=F14H12.3; ORFNames=F14H12.3;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851915;
 RG WormBase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Nelson J., Gattung S., R Wilson.;
 RT "The sequence of C. elegans cosmid F14H12.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.H.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC006630; AAK68125.1; -.
 DR HSP; P07996; ILSL.

DR WormBase; WBGene00017471; F14H12.3.

DR WormPep; F14H12.3; CE07063.

DR InterPro; IPR000884; TSP1.

DR InterPro; IPR000885; TSP_1.

DR Pfam; PF00090; TSP_1; 3_1.

DR PRINTS; PRO1705; TSP1REPEAT.

DR SMART; SM00209; TSP1; 3.

DR PROSITE; PS50092; TSP1; 3.

KW Hypothetical protein.

SQ SEQUENCE 257 AA; 26512 MW; 9B052A0D07F2BEFF CRC64;

Query Match 67.8%; Score 40; DB 2; Length 257;

Best Local Similarity 50.0%; Pred. No. 6.2;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXXXXXXCG 17
 |||||
 Db 145 WSWWSACSVTCG 156

RESULT 7

Q8BVE5 PRELIMINARY; PRT; 478 AA.
 AC Q8BVE5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mus musculus adult male adrenal gland cDNA, RIKEN full-length enriched
 DE library, clone:7330442G16 product:sema domain, seven thrombospondin
 DE repeats (type 1 and type 1-like), transmembrane domain (TM) and short
 DE cytoplasmic domain, (semaphorin) 5B, full insert sequence.
 DE (Fragment).
 DE OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
 RA The FANTOM Consortium,
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,

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RA Sumi N., Iehli Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA "RIKEN Integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RN SEQUENCE FROM N.A.
RP STRAIN=CS7BL/6J; TISSUE=Adrenal gland;
RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanganaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Iehli Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numata K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Shiraki T., Sogabe Y., Tagami M.,
RA Sasaki D., Shibata K., Shinagawa A., Takaku-Akai H., Tanaka T.,
RA Tagawa A., Takahashi F., Takaku-Akai H., Muramatsu M., Hayashizaki Y.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK078659; BAC37350.1; -.
DR HSP; P07996; ILSL.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP 1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1.5.
DR PROSITE; PS50092; TSP1; 5.
FT Transmembrane.
KW NON TER
FT SEQUENCE 478 AA; 51394 MW; F4A9DF173F0A376 CRC64;
SQ
Query Match 67.8%; Score 40; DB 2; Length 478;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 WSXXXCSXXCG 17
Db 19 WSSWAQCTSCG 30
RESULT 8
ID Q62PQ8 PRELIMINARY; PRT; 632 AA.
AC Q62PQ8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKIAA1445 protein (Fragment).
GN Name=MKIAA1445;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryonic tail;
RC PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saka Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries."
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129362; BAC98172.1; -.
DR GO; GO:0005615; C: extracellular space; TAS.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR InterPro; IPR003659; Plexin-like.

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DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP 1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF00090; TSP 1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00209; TSP1; 5.
DR PROSITE; PS50092; TSP1; 5.
FT NON TER
FT SEQUENCE 632 AA; 69037 MW; 78CD7F28C3FF3E7 CRC64;
SQ
Query Match 67.8%; Score 40; DB 2; Length 632;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 WSXXXCSXXCG 17
Db 151 WSSWAQCTSCG 162
RESULT 9
ID Q22580 PRELIMINARY; PRT; 872 AA.
AC Q22580;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAR-2002 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T19D2.1
GN Name=T19D2.1; ORFNames=T19D2.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC Bentley D.;
RT "The sequence of C. elegans cosmid T19D2."
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RP Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U42846; AAA83600.2; -.
DR PIR; T16892; T16892.
DR HSP; P07996; ILSL.
DR WormBase; WBGene00020567; T19D2.1.
DR WormPep; T19D2.1; CE30185.
DR GO; GO:0004222; F: metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P: proteolysis and peptidolysis; IEA.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR00884; TSP1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP 1; 4.
DR SMART; SM00209; TSP1; 4.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50092; TSP1; 4.

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DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 872 AA; 98040 MW; 1BA1D480AEFOED15 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 872;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
|||
Db 831 WSSWSCSTKCG 842

RESULT 10
SMSA_MOUSE
ID SM5A_MOUSE STANDARD; PRT; 1077 AA.
AC Q62217;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Semaphorin 5A precursor (Semaphorin F) (Sema F).
GN Name=Sema5a; Synonyms=SemaF, SemaF;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI;
RX MEDLINE=96414430; PubMed=8817451; DOI=10.1016/0925-4773(96)00525-4;
RA Adams R.H., Bez H., Puechel A.W.;
RT "A novel class of murine semaphorins with homology to thrombospondin
RL Mech. Dev. 57:33-45(1996).
CC -|- FUNCTION: May act as positive axonal guidance cues.
CC -|- SUBUNIT: Binds PLXNB3 (By similarity).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- TISSUE SPECIFICITY: In adult, detected in liver, brain, kidney,
CC heart, lung and spleen.
CC -|- DEVELOPMENTAL STAGE: Differentially expressed in embryonic and
CC adult tissues. Its abundance decreases from E10 to birth.
CC -|- SIMILARITY: Belongs to the semaphorin family.
CC -|- SIMILARITY: Contains 1 Sema domain.
CC -|- SIMILARITY: Contains 7 TSP type-1 domains.

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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR ENBL; X97817; CAA66397.1; -;
DR HSSP; P07996; 1LSL.
DR MGI; MGI:107556; Sema5a.
DR GO; GO:0016021; C:integral to membrane; IDA.
DR GO; GO:0008046; F:axon guidance receptor activity; IDA.
DR GO; GO:0007411; P:axon guidance; IMP.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin-like.
DR InterPro; IPR001627; Sema.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; TSP_1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR SMART; SM00209; TSP1; 6.
DR PROSITE; PSS1004; Sema; 1.
DR PROSITE; PSS0092; TSP1; 6.

KW Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 1077 Semaphorin 5A.
FT DOMAIN 22 971 Extracellular (Potential).
FT TRANSMEM 972 992 Potential.
FT DOMAIN 993 1077 Cytoplasmic (Potential).
FT DOMAIN 35 484 Sema.
FT DOMAIN 540 593 TSP type-1 1.
FT DOMAIN 595 651 TSP type-1 2.
FT DOMAIN 653 702 TSP type-1 3.
FT DOMAIN 707 765 TSP type-1 4.
FT DOMAIN 784 839 TSP type-1 5.
FT DOMAIN 841 896 TSP type-1 6.
FT DOMAIN 897 944 TSP type-1 7.
FT DISULFID 104 114 By similarity.
FT DISULFID 131 140 By similarity.
FT DISULFID 278 320 By similarity.
FT DISULFID 487 504 By similarity.
FT DISULFID 496 513 By similarity.
FT CARBOHYD 147 147 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 168 168 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 277 277 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 323 323 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 367 367 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 717 717 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 933 933 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1077 AA; 120826 MW; EDAB0DDDA42789FF CRC64;

Query Match 67.8%; Score 40; DB 1; Length 1077;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
|||
Db 847 WSSWSCSTKCG 858

RESULT 11
Q6PCK8 PRELIMINARY; PRT; 1088 AA.
ID Q6PCK8
AC Q6PCK8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68835 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2]

SEQUENCE FROM N.A.

TISSUE=Embryo;

MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative." Dev. Dyn. 225:384-391 (2002).

[3]

SEQUENCE FROM N.A.

TISSUE=Embryo;

Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

EMBL; BC059288; AAH59288.1; -.

GO: GO:0016020; C:membrane; IEA.

GO: GO:0004872; F:receptor activity; IEA.

GO: GO:0007275; P:development; IEA.

InterPro; IPR001627; Plexin-like.

InterPro; IPR000884; TSP1.

InterPro; IPR008085; TSP1.

Pfam; PF01437; PSI; 1.

Pfam; PF00090; TSP_1; 5.

PRINTS; PR01705; TSP1REPEAT.

SMART; SM00423; PSI; 1.

SMART; SM00630; Sema; 1.

SMART; SM00209; TSP1; 6.

PROSITE; PS50092; TSP1; 6.

SEQUENCE 1088 AA; 122657 MW; 4DFCD371A7CD8176 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 1088;

Best Local Similarity 50.0%; Pred. No. 21;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXKCG 17

DB 608 WSSWQCSTSCG 619

RESULT 12

ID Q6UY12 PRELIMINARY; PRT; 1092 AA.

AC Q6UY12; (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE SEMA5B.

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.B., Abaya E., Baker K., Baldwin D., Brueh J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J., Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vanden R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;

"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment." Genome Res. 13:2265-2270 (2003).

EMBL; AY358124; AAQ8491.1; -.

GO: GO:0016020; C:membrane; IEA.

GO: GO:0004872; F:receptor activity; IEA.

GO: GO:0007275; P:development; IEA.

InterPro; IPR003659; Plexin-like.

InterPro; IPR001627; Sema.

InterPro; IPR000884; TSP1.

InterPro; IPR008085; TSP_1.

Pfam; PF01437; PSI; 1.

Pfam; PF00090; TSP_1; 5.

PRINTS; PR01705; TSP1REPEAT.

SMART; SM00423; PSI; 1.

SMART; SM00630; Sema; 1.

SMART; SM00209; TSP1; 5.

PROSITE; PS50092; TSP1; 5.

SEQUENCE 1092 AA; 119322 MW; 082BF746687C0AC5 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 1092;

Best Local Similarity 50.0%; Pred. No. 21;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXKCG 17

DB 670 WSSWALCSTSCG 691

RESULT 13

SM5B_HUMAN STANDARD; PRT; 1093 AA.

ID SM5B_HUMAN

AC Q9P283; (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Semaphorin 5B precursor.

GN Name=SEMA5B; Synonyms=KIAA1445;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=20277482; PubMed=10819331;

RA Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro." DNA Res. 7:143-150 (2000).

RL DNA Res. 7:143-150 (2000).

CC -!- FUNCTION: May act as positive axonal guidance cues (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the semaphorin family.

CC -!- SIMILARITY: Contains 1 Sema domain.

CC -!- SIMILARITY: Contains 7 TSP type-1 domains.

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CC EMBL; AB040878; BAB95969.1; ALT_INIT.

DR Genew; HGNC:10737; SEMA5B.

DR InterPro; IPR003659; Plexin-like.

DR InterPro; IPR002165; Plexin_repeat.

DR InterPro; IPR001627; Sema.

```

DR InterPro; IPR000884; TSP1.
DR InterPro; IPR000885; TSP_1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; TSP_1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR SMART; SM00209; TSP1; 5.
DR PROSITE; PS1004; SEMA; 1.
DR PROSITE; PS50092; TSP1; 5.
KW Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 1093 Semaphorin 5B.
FT DOMAIN 20 978 Extracellular (Potential).
FT TRANSMEM 979 999 Potential.
FT DOMAIN 1000 1093 Cytoplasmic (Potential).
FT DOMAIN 45 495 Sema.
FT DOMAIN 551 605 TSP type-1 1.
FT DOMAIN 606 662 TSP type-1 2.
FT DOMAIN 664 713 TSP type-1 3.
FT DOMAIN 721 776 TSP type-1 4.
FT DOMAIN 795 850 TSP type-1 5.
FT DOMAIN 852 907 TSP type-1 6.
FT DOMAIN 908 952 TSP type-1 7.
FT CARBOHYD N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 95 95 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 157 157 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 287 287 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 333 333 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 378 378 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 532 532 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 539 539 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 547 547 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 602 602 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 728 728 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 944 944 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 1093 AA; 119866 MW; F1FDFPB87CEAF0EF CRC64;

Query Match 67.8%; Score 40; DB 1; Length 1093;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXXXXXCG 17
DB 612 WSSWALCSTSCG 623

RESULT 14
SMSB_MOUSE STANDARD; PRT; 1093 AA.
AC Q60519;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Semaphorin 5B precursor (Semaphorin G) (Sema G).
GN Names=Sema5b; Synonyms=SEWAG, SemG;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=NMRI;
RX MEDLINE=96414430; PubMed=8817451; DOI=10.1016/0925-4773(96)00525-4;
RA Adams R.H., Betz H., Puschel A.W.;
RT "A novel class of murine semaphorins with homology to thrombospondin
RT is differentially expressed during early embryogenesis.";
RL Mech. Dev. 57:33-45(1996).
CC -!- FUNCTION: May act as positive axonal guidance cues.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

```

```

CC -!- TISSUE SPECIFICITY: In adult, only detected in brain.
CC -!- DEVELOPMENTAL STAGE: Differentially expressed in embryonic and
CC adult tissues. Its abundance decreases from E10 to birth.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -!- SIMILARITY: Contains 7 TSP type-1 domains.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X97818; CAA65398.1; --
CC HSSP; P07996; ILSL.
CC MGSD; MGI:107555; Sema5b.
CC InterPro; IPR003659; Plexin-like.
CC InterPro; IPR001625; Plexin_repeat.
CC InterPro; IPR001627; Sema.
CC InterPro; IPR000884; TSP1.
CC InterPro; IPR008085; TSP_1.
CC Pfam; PF01437; PSI; 1.
CC Pfam; PF01403; Sema; 1.
CC Pfam; PF00090; TSP_1; 5.
CC PRINTS; PR01705; TSP1REPEAT.
CC SMART; SM00423; PSI; 1.
CC SMART; SM00630; Sema; 1.
CC SMART; SM00209; TSP1; 5.
CC PROSITE; PS1004; SEMA; 1.
CC PROSITE; PS50092; TSP1; 5.
KW Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1093 Semaphorin 5B.
FT DOMAIN 20 978 Extracellular (Potential).
FT TRANSMEM 979 999 Potential.
FT DOMAIN 1000 1093 Cytoplasmic (Potential).
FT DOMAIN 45 495 Sema.
FT DOMAIN 551 605 TSP type-1 1.
FT DOMAIN 606 662 TSP type-1 2.
FT DOMAIN 664 713 TSP type-1 3.
FT DOMAIN 721 776 TSP type-1 4.
FT DOMAIN 795 850 TSP type-1 5.
FT DOMAIN 852 907 TSP type-1 6.
FT DOMAIN 908 952 TSP type-1 7.
FT CARBOHYD N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 95 95 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 157 157 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 287 287 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 333 333 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 378 378 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 532 532 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 539 539 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 547 547 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 602 602 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 728 728 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 944 944 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 1093 AA; 120326 MW; 29E5C9B1E8108717 CRC64;

Query Match 67.8%; Score 40; DB 1; Length 1093;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXXXXXCG 17
DB 612 WSSWALCSTSCG 623

RESULT 15
Q7QC32

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ID Q7QC32 PRELIMINARY; PRT; 1093 AA.
AC Q7QC32;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ebip1179 (Fragment).
GN Name=ebig1179; ORFNames=ENSANGG00000001015;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100859; EAA07529.1; -.
DR HSSP; Q92854; IOLZ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002165; plexin_repeat.
DR InterPro; IPR001627; Sema.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; TSP_1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR PROSITE; PS50092; TSP1; 5.
FT NON_TER . 1
FT NON_TER 1093 1093
SQ SEQUENCE 1093 AA; 118842 MW; 2DB86BEC7CB42230 CRC64;
Query Match . 67.8%; Score 40; DB 2; Length 1093;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 WSXXXGCSXXCG 17
Db 586 WSAWSACSQTG 597
Search completed: April 1, 2005, 13:59:24
Job time : 139.696 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:43:07 ; Search time 30.6087 Seconds
(without alignments)
69.156 Million cell updates/sec

Title: US-09-462-909D-9

Perfect score: 59

Sequence: 1 XXXXXWSXXXCSXXCGXXXXX 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

.Database :

PIR 79:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	67.8	860	2	T16892
2	40	67.8	1170	1	TSHUP1
3	40	67.8	1170	2	A40558
4	39	66.1	206	2	A45517
5	39	66.1	610	2	T16761
6	39	66.1	654	2	T29247
7	39	66.1	712	2	A45638
8	39	66.1	724	2	A48569
9	39	66.1	984	2	T00326
10	39	66.1	1444	2	T18856
11	39	66.1	1522	2	T00028
12	39	66.1	2098	2	T18397
13	38	64.4	788	2	T25061
14	38	64.4	803	2	A47723
15	38	64.4	807	2	A38152
16	38	64.4	957	2	T15976
17	38	64.4	1074	2	JCS928
18	38	64.4	1172	1	TSHUP2
19	38	64.4	1172	2	A42587
20	38	64.4	1178	1	A39804
21	38	64.4	1184	2	T09484
22	38	64.4	1205	2	T18517
23	38	64.4	1584	2	T00026
24	37	62.7	437	2	S05478
25	37	62.7	551	2	T16557
26	37	62.7	805	2	T34212
27	37	62.7	1360	2	T33922
28	37	62.7	1572	2	T00027
29	35	59.3	1059	2	T22545

plectoxin X - spid
TRAP-C2 protein -
hypothetical prote
hypothetical prote
hypothetical prote
unc-5 protein - Ca
hypothetical prote
hypothetical lon
hypothetical prote
thrombospondin-rel
sporozoite surface
hypothetical prote
hypothetical prote
hypothetical prote
propordin precurs
hypothetical prote
hypothetical prote

ALIGNMENTS

RESULT 1

T16892

hypothetical protein T19D2.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T16892

R;Bentley, D.

submitted to the EMBL Data Library, December 1995

A;Description: The sequence of C. elegans cosmid T19D2.

A;Reference number: Z18599

A;Accession: T16892

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-860 <BEN>

A;Cross-references: UNIPROT:Q22580; EMBL:U42846; MID:g1125810; PIDN:AAA8361

C;Genetics:

A;Gene: CBSP:T19D2.1

A;Introns: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 581/3

Query Match 67.8%; Score 40; DB 2; Length 860;

Best Local Similarity 50.0%; Pred. No. 4.2;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXXCG 17

DB 831 WSWSSCSYKCG 842

RESULT 2

TSHUP1

thrombospondin 1 precursor - human

C;Species: Homo sapiens (man)

C;Date: 23-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: A26155; A34274; A30140; A25812; A05172; A42927

R;Lawler, J.; Hynes, R.O.

J. Cell Biol. 103, 1635-1648, 1986

A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple ca

A;Reference number: A26155; MUID:87057617; PMID:2430973

A;Accession: A26155

A;Molecule type: mRNA

A;Residues: 1-1170 <LAH>

A;Cross-references: UNIPROT:P07996; GB:X04665; MID:g37137; PIDN:CAA28370.1; PID:g37138

A;Note: parts of this sequence, including the amino end of the mature protein, were deter

R;Lawler, J.; Hynes, R.O.

J. Biol. Chem. 264, 11222-11227, 1989

A;Title: Characterization of the promoter region of the human thrombospondin gene. DNA se

A;Reference number: A34274; MUID:89291870; PMID:2544587

A;Accession: A34274

A;Molecule type: DNA

A;Residues: 1-166 <LAH>

A;Cross-references: GB:J04835

R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, F.

R.Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
Genomics 11, 587-600, 1991
A:Title: Characterization of the murine thrombospondin gene.
A:Accession: A40558; MUID:92128941; PMID:1774063
A:Accession: A40558
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1170 <LAW>
A:Cross-references: UNIPROT:P35441; GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M62453;
GB:M62464; GB:M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:G51186
R:Bornstein, P.; Alfai, D.; Devarayalu, S.; Framson, P.; Li, P.
J. Biol. Chem. 265, 16691-16698, 1990
A:Title: Characterization of the mouse thrombospondin gene and evaluation of the role of
A:Reference number: A37905; MUID:90375546; PMID:2398070
A:Accession: A37905
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <BOR>
A:Cross-references: GB:J05605; GB:J05606; NID:G20191; PIDN:AAA040431.1; PID:G554390
R:Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A:Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A:Reference number: A42587; MUID:92147683; PMID:1371115
A:Accession: B42587
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1152, 'P', 1154-1170 <LAH>
A:Cross-references: GB:M87276
A:Note: sequence extracted from NCBI backbone (NCBIP:81501)
R:Chen, H.; Aeschlimann, D.; Nowien, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A:Title: Expression and initial characterization of recombinant mouse thrombospondin 1 a
A:Reference number: S68787; MUID:96234006; PMID:8654563
A:Accession: S68787
A:Molecule type: protein
A:Residues: 19-26, 'X', 28-37 <CHE>
C:Complex: homotrimer, disulfide linked
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von
C:Keywords: calcium binding; glycoprotein; homotrimer
P:1-18/Domain: signal sequence #status predicted <SIG>
P:19-1170/Product: thrombospondin 1 #status predicted <MAT>
P:317-375/Domain: von Willebrand factor type C repeat homology <VWC>
P:378-429/Domain: thrombospondin type 1 repeat homology <THR1>
P:434-490/Domain: thrombospondin type 1 repeat homology <THR2>
P:491-547/Domain: thrombospondin type 1 repeat homology <THR3>
P:551-586/Domain: EGF homology <EGF>
P:248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.8%; Score 40; DB 2; Length 1170;
Best Local Similarity 50.0%; Pred. No. 5.2;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WSXXXXGSGXXCG 17
Db 385 WSEWTSGSATCG 396

RESULT 4
A45517
coccioidis-related antigen - Eimeria tenella (fragment)
N:Alternate names: thrombospondin-related antigen, 100K
C:Species: Eimeria tenella
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
C:Accession: A45517; S27818
R:Clarke, L.E.; Tomley, F.M.; Wisner, M.H.; Foulds, I.J.; Boursnell, M.E.G.
Mol. Biochem. Parasitol. 41, 269-280, 1990
A:Title: Regions of an Eimeria tenella antigen contain sequences which are conserved in
A:Reference number: A45517; MUID:90377296; PMID:2204833
A:Accession: A45517
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <CLA>
A:Cross-references: UNIPROT:Q24927; GB:M32988; NID:G158870; PID:G158871

F;136-198/Domain: thrombospondin type 1 repeat homology <THR5>

Query Match 66.1%; Score 39; DB 2; Length 206;
Best Local Similarity 50.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCXXKCG 17
DB 21 WSEWTECSATCG 32

RESULT 5

T16761

hypothetical protein R151.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Dec-2002

C;Accession: T16761

R;Fulton, L.

submitted to the EMBL Data Library, February 1994

A;Description: The sequence of C. elegans cosmid R151.

A;Reference number: S44639

A;Accession: T16761

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-610 <FUL>

A;Cross-references: EMBL:U00036; NID:G458996; PID:G459001; PIDN:AAA50653.1; CESP:R151.5

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:R151.5

A;Introns: 68/3; 120/1; 151/1; 307/1; 448/2; 525/2; 567/2; 592/2

C;Superfamily: metalloproteinase hch-1; astacin homology

Query Match

Best Local Similarity 66.1%; Score 39; DB 2; Length 610;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCXXKCG 17
DB 496 WSPWTACSATCG 507

RESULT 6

T29247

hypothetical protein F09F9.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T29247

R;Minx, P.; Hawkins, J.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of C. elegans cosmid F09F9.

A;Reference number: Z20594

A;Accession: T29247

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-654 <MIN>

A;Cross-references: UNIPROT:Q19284; EMBL:U40959; PIDN:AAA81764.1; CESP:F09F9.4

C;Genetics:

A;Gene: CESP:F09F9.4

A;Introns: 89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1; 523/1; 558/2; 596/2

Query Match

Best Local Similarity 66.1%; Score 39; DB 2; Length 654;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCXXKCG 17
DB 322 WSEWSACSETCG 333

RESULT 7

A45638

immunodominant microneme protein Etp100 - Eimeria tenella

C;Species: Eimeria tenella

C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A45638

R;Tomley, P.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.

Mol. Biochem. Parasitol. 49, 277-288, 1991

A;Title: Sequence of the gene encoding an immunodominant microneme protein of Eimeria ter

A;Reference number: A45638; MUID:92131084; PMID:1775171

A;Accession: A45638

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-712 <TOM>

A;Cross-references: UNIPROT:O43981; GB:AF032905; GB:M73495; NID:G270732; PIDN:AAD03350.1

A;Note: sequence extracted from NCBI backbone (NCBIN:77752, NCBIIP:77756)

F;48-218/Domain: von Willebrand factor type A repeat homology <VWA1>

F;238-296/Domain: thrombospondin type 1 repeat homology <THR1>

F;309-371/Domain: thrombospondin type 1 repeat homology <THR2>

F;372-432/Domain: thrombospondin type 1 repeat homology <THR3>

F;433-493/Domain: thrombospondin type 1 repeat homology <THR4>

F;494-556/Domain: thrombospondin type 1 repeat homology <THR5>

F;560-610/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match

Best Local Similarity 66.1%; Score 39; DB 2; Length 712;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCXXKCG 17
DB 379 WSEWTECSATCG 390

RESULT 8

A48569

antigen Eml00 - Eimeria maxima

C;Species: Eimeria maxima

C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A48569

R;Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G.

Mol. Biochem. Parasitol. 57, 171-174, 1993

A;Title: Sequence of a major Eimeria maxima antigen homologous to the Eimeria tenella mic

A;Reference number: A48569; MUID:93149203; PMID:8426611

A;Accession: A48569

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-724 <PAS>

A;Cross-references: UNIPROT:Q04588; GB:M99058; NID:G158890; PID:G158891

F;45-218/Domain: sequence extracted from NCBI backbone (NCBIN:123776, NCBIIP:123777)

F;238-296/Domain: von Willebrand factor type A repeat homology <VWA2>

F;309-371/Domain: thrombospondin type 1 repeat homology <THR1>

F;372-432/Domain: thrombospondin type 1 repeat homology <THR2>

F;433-493/Domain: thrombospondin type 1 repeat homology <THR3>

F;494-556/Domain: thrombospondin type 1 repeat homology <THR4>

F;560-610/Domain: thrombospondin type 1 repeat homology <THR5>

Query Match

Best Local Similarity 66.1%; Score 39; DB 2; Length 724;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCXXKCG 17
DB 379 WSDWSDCSATCG 390

RESULT 9

T00326

hypothetical protein KIAA0550 - human

C;Species: Homo sapiens (man)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 15-Mar-2004

C;Accession: T00326

R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.

DNA Res. 5, 31-39, 1998

A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complete

A;Reference number: Z14086; MUID:98290545; PMID:9628581

A;Accession: T00326

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-984 <NAG>
A;Cross-references: EMBL:AB011122; NID:g3043623; PIDN:BAA25476.1; PID:g3043624
A;Experimental source: brain
C;Genetics:
A;Note: KIA00550
F;344-398/Domain: thrombospondin type 1 repeat homology <THR3>
Query Match 66.1%; Score 39; DB 2; Length 984;
Best Local Similarity 50.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
QY 6 WXXXXXCSXXCG 17
DB 297 WSWSTCSVTCG 308
RESULT 10
T18856
angiogenesis inhibitor homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18856; T24653
R;McMurray, A.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19031
A;Accession: T18856
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1444 <WIL>
A;Cross-references: UNIPROT:Q8MYA8; EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN000028; CESP:CD
A;Experimental source: clone C02B4
R;McMurray, A.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19917
A;Accession: T24653
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1444 <W12>
A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN000028; CESP:C02B4.1
C;Genetics:
A;Gene: CESP:C02B4.1
A;Map position: X
A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566/3
Query Match 66.1%; Score 39; DB 2; Length 1444;
Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
QY 6 WXXXXXCSXXCG 17
DB 696 WSSWSECSVSG 707
RESULT 11
T00028
brain-specific angiogenesis inhibitor 3 - human
N;Alternate names: BAI3 protein
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00028
R;Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.
Cytoget. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-
A;Reference number: Z14066; MUID:98194217; PMID:9533023
A;Accession: T00028
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1522 <SHI>
A;Cross-references: UNIPROT:O60242; EMBL:AB005299; NID:g3021700; PIDN:BAA25363.1; PID:g3
A;Experimental source: brain

C;Genetics:
A;Gene: GDB:BAI3
A;Cross-references: GDB:9838090; OMIM:602684
A;Map position: 6q12-6q12
F;344-398/Domain: thrombospondin type 1 repeat homology <THR3>
Query Match 66.1%; Score 39; DB 2; Length 1522;
Best Local Similarity 50.0%; Pred. No. 9.5;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
QY 6 WXXXXXCSXXCG 17
DB 297 WSWSTCSVTCG 308
RESULT 12
T18397
protein CTRP - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18397
R;Protein, F.; Triglia, T.; Cowman, A.F.
Mol. Biochem. Parasitol. 74, 129-142, 1995
A;Title: Molecular cloning of a gene from Plasmodium falciparum that codes for a protein
A;Reference number: Z18926; MUID:96360471; PMID:8719155
A;Accession: T18397
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2098 <TRO>
A;Cross-references: UNIPROT:Q25757; EMBL:U34363; NID:g1098897; PID:g1098898; PIDN:AAC469
Query Match 66.1%; Score 39; DB 2; Length 2098;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
QY 6 WXXXXXCSXXCG 17
DB 1644 WSDWSSCSKTCG 1655
RESULT 13
T25061
hypothetical protein T21B6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25061
R;Cottage, A.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19975
A;Accession: T25061
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-788 <WIL>
A;Cross-references: UNIPROT:Q22631; EMBL:Z68011; PIDN:CAA92014.1; GSPDB:GN000028; CESP:T2
A;Experimental source: clone T21B6
C;Genetics:
A;Gene: CESP:T21B6.3
A;Map position: X
A;Introns: 20/1; 47/1; 76/1; 152/1; 735/2; 754/2
Query Match 64.4%; Score 38; DB 2; Length 788;
Best Local Similarity 50.0%; Pred. No. 9.3;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
QY 6 WXXXXXCSXXCG 17
DB 461 WSDWSTCSCTCG 472
RESULT 14
A4723
F-spondin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)

C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A47723
R:Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A:Title: Ectopic neural expression of a floor plate marker in frog embryos injected with
A:Reference number: A47723; MUID:93376785; PMID:8367492
A:Accession: A47723
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-803 <RUI>
A:Cross-references: UNIPROT:P35447; GB:L09123; NID:G409244; PIDN:AAA19105.1; PID:G409245
C:Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;435-489/Domain: thrombospondin type 1 repeat homology <THR2>
F;607-662/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 64.4%; Score 38; DB 2; Length 803;
Best Local Similarity 50.0%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXXCG 17
Db 614 WSEWSDCSVTCG 625

RESULT 15
A38152
F-spondin - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A38152
R:Klar, A.; Baldassare, M.; Jessell, T.M.
Cell 69, 95-110, 1992
A:Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secreted
A:Reference number: A38152; MUID:92208952; PMID:1555244
A:Accession: A38152
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-807 <KLA>
A:Cross-references: UNIPROT:P35446; GB:M8469; NID:G204176; PIDN:AAA41174.1; PID:G204177
A:Experimental source: embryo floor plate
C:Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;441-495/Domain: thrombospondin type 1 repeat homology <THR2>
F;500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F;557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F;613-666/Domain: thrombospondin type 1 repeat homology <THR1>
F;667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F;753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 64.4%; Score 38; DB 2; Length 807;
Best Local Similarity 50.0%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXXCG 17
Db 620 WSEWSDCSVTCG 631

Search completed: April 1, 2005, 14:00:31
Job time : 31.6087 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:59:39 ; Search time 113.348 Seconds
(without alignments)
64.360 Million cell updates/sec

Title: US-09-462-909D-9
Perfect score: 59
Sequence: 1 XXXXXWSXXXCSCXXCGXXXXX 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pap.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pap.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pap.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pap.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pap.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pap.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pap.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	67.8	23	14	US-10-042-696-11
2	40	67.8	50	10	US-09-373-658-6
3	40	67.8	50	11	US-09-989-687-6
4	40	67.8	50	15	US-10-019-065A-6
5	40	67.8	51	17	US-10-883-144-35
6	40	67.8	143	15	US-10-276-774-1454
7	40	67.8	170	15	US-10-419-462-43
8	40	67.8	170	16	US-10-296-733-20
9	40	67.8	170	17	US-10-782-968-43
10	40	67.8	218	13	US-10-036-869-1
11	40	67.8	397	17	US-10-454-246-20
12	40	67.8	401	15	US-10-190-115-111
13	40	67.8	401	15	US-10-190-115-114

14	40	67.8	401	15	US-10-190-115-116	Sequence 116, App
15	40	67.8	401	15	US-10-190-115-118	Sequence 118, App
16	40	67.8	401	17	US-10-454-246-10	Sequence 10, Appl
17	40	67.8	401	17	US-10-454-246-12	Sequence 12, Appl
18	40	67.8	401	17	US-10-454-246-14	Sequence 14, Appl
19	40	67.8	401	17	US-10-454-246-16	Sequence 16, Appl
20	40	67.8	432	17	US-10-741-600-1020	Sequence 1020, Ap
21	40	67.8	432	17	US-10-741-600-1022	Sequence 1022, Ap
22	40	67.8	441	13	US-10-036-869-3	Sequence 3, Appli
23	40	67.8	466	9	US-09-925-301-1047	Sequence 1047, Ap
24	40	67.8	606	14	US-10-234-432-70	Sequence 70, Appl
25	40	67.8	831	11	US-09-938-853A-97	Sequence 97, Appl
26	40	67.8	831	11	US-09-939-853A-98	Sequence 98, Appl
27	40	67.8	939	9	US-09-854-845-16	Sequence 16, Appl
28	40	67.8	939	17	US-10-833-509-16	Sequence 16, Appl
29	40	67.8	954	9	US-09-854-845-14	Sequence 14, Appl
30	40	67.8	954	17	US-10-833-509-14	Sequence 14, Appl
31	40	67.8	1034	9	US-09-854-845-6	Sequence 6, Appli
32	40	67.8	1034	17	US-10-833-509-6	Sequence 6, Appli
33	40	67.8	1049	9	US-09-854-845-2	Sequence 2, Appli
34	40	67.8	1049	17	US-10-833-509-2	Sequence 2, Appli
35	40	67.8	1077	15	US-10-190-115-43	Sequence 43, Appl
36	40	67.8	1077	15	US-10-369-072-43	Sequence 43, Appl
37	40	67.8	1078	9	US-09-854-845-8	Sequence 8, Appli
38	40	67.8	1078	17	US-10-833-509-8	Sequence 8, Appli
39	40	67.8	1092	14	US-10-245-752-96	Sequence 96, Appl
40	40	67.8	1092	14	US-10-245-859-96	Sequence 96, Appl
41	40	67.8	1092	14	US-10-245-103-96	Sequence 96, Appl
42	40	67.8	1092	14	US-10-245-107-96	Sequence 96, Appl
43	40	67.8	1092	14	US-10-245-143-96	Sequence 96, Appl
44	40	67.8	1092	14	US-10-245-771-96	Sequence 96, Appl
45	40	67.8	1092	14	US-10-245-851-96	Sequence 96, Appl

ALIGNMENTS

RESULT 1
US-10-042-696-11
; Sequence 11, Application US/10042696
; Publication No. US20030171298A1
; GENERAL INFORMATION:
; APPLICANT: Tuszyński, George
; APPLICANT: Williams, Taffy
; APPLICANT: Actor, Paul
; TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT THROMBOSPONDIN ACT
; FILE REFERENCE: 07206-0021
; CURRENT APPLICATION NUMBER: US/10/042,696
; CURRENT FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver 2.0
; SEQ ID NO 11
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic fragment/analog of thrombospondin
; OTHER INFORMATION: thrombospondin
US-10-042-696-11

Query Match
Best Local Similarity 50.0%
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WXXXXCSCXXCG 17
Db 4 WSEWTSCSTSCG 15

RESULT 2
US-09-373-658-6
; Sequence 6, Application US/09373658
; Publication No. US20030092900A1

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Isolated type 1 thrombospondin domain sequence
US-10-019-065A-6

Query Match      67.8%; Score 40; DB 15; Length 50;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 WXXXXXCSXXCG 17
      ||| |||
Db      6 WSEWTSCTSCG 17

RESULT 5
US-10-883-144-35
; Sequence 35, Application US/10883144
; Publication No. US20050054829A1
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; APPLICANT: Wiley, Steven R.
; APPLICANT: Vakili, Jalaleddin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO TSP-30a, b, c AND d
; FILE REFERENCE: 3474-A
; CURRENT APPLICATION NUMBER: US/10/883,144
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US 60/489,409
; PRIOR FILING DATE: 2003-07-22
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-883-144-35

Query Match      67.8%; Score 40; DB 17; Length 51;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 WXXXXXCSXXCG 17
      ||| |||
Db      7 WSEWTSCTSCG 18

RESULT 6
US-10-276-774-1454
; Sequence 1454, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y. Tom et al
; TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1454
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-1454

Query Match      67.8%; Score 40; DB 15; Length 143;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-373-658-6

Query Match      67.8%; Score 40; DB 10; Length 50;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 WXXXXXCSXXCG 17
      ||| |||
Db      7 WSEWTSCTSCG 18

RESULT 3
US-09-989-687-6
; Sequence 6, Application US/09989687
; Publication No. US2004002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070000
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-989-687-6

Query Match      67.8%; Score 40; DB 11; Length 50;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 WXXXXXCSXXCG 17
      ||| |||
Db      7 WSEWTSCTSCG 18

RESULT 4
US-10-019-065A-6
; Sequence 6, Application US/10019065A
; Publication No. US20040086501A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Corporation
; TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
; FILE REFERENCE: MSB-7265-PCT
; CURRENT APPLICATION NUMBER: US/10/019,065A
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/266,300.
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 50

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QY 6 WSXXXXCSXXCG 17
|||
Db 89 WSSWALCSTSCG 100

RESULT 7

US-10-419-462-43
; Sequence 43, Application US/10419462
; Publication No. US20040053392A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Williams
; APPLICANT: Williams, Kevin J.
; TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for
; TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
; FILE REFERENCE: W1107-20005
; CURRENT APPLICATION NUMBER: US/10/419,462
; CURRENT FILING DATE: 2003-04-17
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 43
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thrombospondin Region plus Domain of type 1 repeats
US-10-419-462-43

Query Match 67.8%; Score 40; DB 15; Length 170;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
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Db 7 WSEWTSCTSCG 18

RESULT 8

US-10-296-733-20
; Sequence 20, Application US/10296733
; Publication No. US20040110131A1
; GENERAL INFORMATION:
; APPLICANT: Beth Israel Deaconess Medical Center
; APPLICANT: Lawler, John W.
; TITLE OF INVENTION: Thrombospondin-1 Type 1 Repeat
; FILE REFERENCE: 1440.2009002
; CURRENT APPLICATION NUMBER: US/10/296,733
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/207,994
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-733-20

Query Match 67.8%; Score 40; DB 16; Length 170;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
|||
Db 7 WSEWTSCTSCG 18

RESULT 9

US-10-782-968-43
; Sequence 43, Application US/10782968
; Publication No. US20050065324A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Williams

; APPLICANT: Williams, Kevin J.
; TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for
; TITLE OF INVENTION: Cancer and Generation of Antibodies and Other Binding Agents
; FILE REFERENCE: W1107-20005
; CURRENT APPLICATION NUMBER: US/10/782,968
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/10/419,462
; PRIOR FILING DATE: 2003-04-21
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 43
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thrombospondin Region plus Domain of type 1 repeats
US-10-782-968-43

Query Match 67.8%; Score 40; DB 17; Length 170;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
|||
Db 7 WSEWTSCTSCG 18

RESULT 10
US-10-036-869-1
; Sequence 1, Application US/10036869
; Publication No. US20020151516A1
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A.
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; THERAPY

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19899

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/036,869
FILING DATE: 29-No. US20020151516A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: McMorrow Jr., Robert G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-036-869-1
Query Match 67.8%; Score 40; DB 13; Length 218;
Best Local Similarity 50.0%; Pred. No. 34;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXCG 17
 Db 85 WSEWTSCTSCG 96

RESULT 11

US-10-454-246-20
 ; Sequence 20, Application US/10454246
 ; Publication No. US20050053930A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, et al.
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 ; FILE REFERENCE: 21402-589 B
 ; CURRENT APPLICATION NUMBER: US/10/454,246
 ; CURRENT FILING DATE: 2003-06-03
 ; PRIOR APPLICATION NUMBER: 09/898,994
 ; PRIOR FILING DATE: 2001-07-03
 ; PRIOR APPLICATION NUMBER: 60/218,903
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 10/016,248
 ; PRIOR FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: 60/255,648
 ; PRIOR FILING DATE: 2000-12-14
 ; PRIOR APPLICATION NUMBER: 10/028,248
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/256,619
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: 10/044,564
 ; PRIOR FILING DATE: 2002-01-11
 ; PRIOR APPLICATION NUMBER: 60/261,013
 ; PRIOR FILING DATE: 2001-01-11
 ; PRIOR APPLICATION NUMBER: 10/136,071
 ; PRIOR FILING DATE: 2002-05-01
 ; PRIOR APPLICATION NUMBER: 60/289,087
 ; PRIOR FILING DATE: 2001-05-07
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 339
 ; SOFTWARE: CuraSeqList version 0.1
 ; SEQ ID NO 20
 ; LENGTH: 397
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Domain
 US-10-454-246-20

Query Match 67.8%; Score 40; DB 17; Length 397;
 Best Local Similarity 50.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXCG 17
 Db 58 WSSWALCSTSCG 69

RESULT 12

US-10-190-115-111
 ; Sequence 111, Application US/10190115
 ; Publication No. US20030207394A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alsbrook, John P. II
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Mezick, Amanda J.
 ; APPLICANT: Padigar, Muralidhara

; APPLICANT: Patturajan, Meera
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Shen, Lei
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Spaderna, Steven K.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Szekeres, Edward S. Jr.
 ; APPLICANT: Taupier, Raymond J. Jr.
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Voss, Edward Z.
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-050 CIP
 ; CURRENT APPLICATION NUMBER: US/10/190,115
 ; CURRENT FILING DATE: 2003-02-10
 ; PRIOR APPLICATION NUMBER: 60/303,168
 ; PRIOR FILING DATE: 2001-07-05
 ; PRIOR APPLICATION NUMBER: 60/368,996
 ; PRIOR FILING DATE: 2002-04-01
 ; PRIOR APPLICATION NUMBER: 60/386,816
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: 60/215,854
 ; PRIOR FILING DATE: 2000-07-03
 ; PRIOR APPLICATION NUMBER: 60/215,856
 ; PRIOR FILING DATE: 2000-07-03
 ; PRIOR APPLICATION NUMBER: 60/215,902
 ; PRIOR FILING DATE: 2000-07-03
 ; PRIOR APPLICATION NUMBER: 60/216,585,
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/216,586
 ; PRIOR FILING DATE: 2001-07-07
 ; PRIOR APPLICATION NUMBER: 60/216,722
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/218,622
 ; PRIOR FILING DATE: 2000-07-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 136
 ; SOFTWARE: CuraSeqList version 0.1
 ; SEQ ID NO 111
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-190-115-111

Query Match 67.8%; Score 40; DB 15; Length 401;
 Best Local Similarity 50.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXCG 17
 Db 60 WSSWALCSTSCG 71

RESULT 13

US-10-190-115-114
 ; Sequence 114, Application US/10190115
 ; Publication No. US20030207394A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alsbrook, John P. II
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Mezick, Amanda J.
 ; APPLICANT: Padigar, Muralidhara
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Shen, Lei

/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Shinkets, Richard A.
/ APPLICANT: Spaderna, Steven K.
/ APPLICANT: Spytek, Kimberly A.
/ APPLICANT: Szekeres, Edward S. Jr.
/ APPLICANT: Taupier, Raymond J. Jr.
/ APPLICANT: Tchernev, Velizar T.
/ APPLICANT: Zerhusen, Bryan D.
/ APPLICANT: Voss, Edward Z.
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-050 CIP
/ CURRENT APPLICATION NUMBER: US/10/190,115
/ CURRENT FILING DATE: 2003-02-10
/ PRIOR APPLICATION NUMBER: 60/303,168
/ PRIOR FILING DATE: 2001-07-05
/ PRIOR APPLICATION NUMBER: 60/368,996
/ PRIOR FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: 60/386,816
/ PRIOR FILING DATE: 2002-06-07
/ PRIOR APPLICATION NUMBER: 60/215,854
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,856
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,902
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/216,585,
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/216,586
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/216,586
/ PRIOR FILING DATE: 2001-07-07
/ PRIOR APPLICATION NUMBER: 60/216,722
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/218,622
/ PRIOR FILING DATE: 2000-07-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 136
/ SOFTWARE: CuraseqList version 0.1
/ SEQ ID NO 114
/ LENGTH: 401
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-190-115-114.

Query Match 67.8%; Score 40; DB 15; Length 401;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
DB 60 WSSWALCSTSCG 71

RESULT 14
US-10-190-115-116
/ Sequence 116, Application US/10190115
/ Publication No. US20030207394A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsobrook, John P. II
/ APPLICANT: Boldog, Ferenc L.
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Grosse, William M.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Ji, Weizhen
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Mezick, Amanda J.
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Shen, Lei
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Shinkets, Richard A.
/ APPLICANT: Spaderna, Steven K.

/ APPLICANT: Spytek, Kimberly A.
/ APPLICANT: Szekeres, Edward S. Jr.
/ APPLICANT: Taupier, Raymond J. Jr.
/ APPLICANT: Tchernev, Velizar T.
/ APPLICANT: Zerhusen, Bryan D.
/ APPLICANT: Voss, Edward Z.
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-050 CIP
/ CURRENT APPLICATION NUMBER: US/10/190,115
/ CURRENT FILING DATE: 2003-02-10
/ PRIOR APPLICATION NUMBER: 60/303,168
/ PRIOR FILING DATE: 2001-07-05
/ PRIOR APPLICATION NUMBER: 60/368,996
/ PRIOR FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: 60/386,816
/ PRIOR FILING DATE: 2002-06-07
/ PRIOR APPLICATION NUMBER: 60/215,854
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,856
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,902
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/216,585,
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/216,586
/ PRIOR FILING DATE: 2001-07-07
/ PRIOR APPLICATION NUMBER: 60/216,722
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/218,622
/ PRIOR FILING DATE: 2000-07-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 136
/ SOFTWARE: CuraseqList version 0.1
/ SEQ ID NO 116
/ LENGTH: 401
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-190-115-116

Query Match 67.8%; Score 40; DB 15; Length 401;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
DB 60 WSSWALCSTSCG 71

RESULT 15
US-10-190-115-118
/ Sequence 118, Application US/10190115
/ Publication No. US20030207394A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsobrook, John P. II
/ APPLICANT: Boldog, Ferenc L.
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Grosse, William Y.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Ji, Weizhen
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Mezick, Amanda J.
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Shen, Lei
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Shinkets, Richard A.
/ APPLICANT: Spaderna, Steven K.
/ APPLICANT: Spytek, Kimberly A.
/ APPLICANT: Szekeres, Edward S. Jr.
/ APPLICANT: Taupier, Raymond J. Jr.

Fri Apr 1 15:03:06 2005

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; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 118
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-190-115-118

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Query Match      67.8%; Score 40; DB 15; Length 401;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY      6 WXXXXXCSXXCG 17
Db      60 WSSWALCSTSCG 71

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Search completed: April 1, 2005, 14:22:18
Job time : 114.348 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 13:44:22 ; Search time 38.7391 Seconds
(without alignments)
42.393 Million cell updates/sec

Title: US-09-462-909D-9

Perfect score: 59

Sequence: 1 XXXXXWSXXXCSCXXCXXXXX 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	40	67.8	23	2	US-08-488-273-5
3	40	67.8	23	3	US-09-197-770B-11
4	40	67.8	23	6	5426100-5
5	40	67.8	23	6	5426100-5
6	40	67.8	218	3	US-08-985-526-1
7	40	67.8	239	5	PCT-US93-01652-1
8	40	67.8	441	3	US-08-985-526-3
9	40	67.8	939	4	US-09-854-845-16
10	40	67.8	954	4	US-09-854-845-14
11	40	67.8	1034	4	US-09-854-845-6
12	40	67.8	1049	4	US-09-854-845-2
13	40	67.8	1078	4	US-09-854-845-8
14	40	67.8	1093	4	US-09-854-845-4
15	40	67.8	1136	4	US-09-854-845-12
16	40	67.8	1151	4	US-09-854-845-10
17	40	67.8	1170	1	US-08-313-288B-20
18	40	67.8	1170	4	US-09-657-472-2
19	39	66.1	120	4	US-09-270-767-32422
20	39	66.1	120	4	US-09-270-767-47639
21	39	66.1	479	4	US-09-270-767-46823
22	39	66.1	677	4	US-09-270-767-58094
23	39	66.1	847	4	US-09-270-767-42783
24	39	66.1	874	3	US-09-369-364A-15
25	39	66.1	997	3	US-09-369-364A-7
26	38	64.4	23	1	US-07-646-531D-5
27	38	64.4	23	2	US-08-488-273-5

28	38	64.4	23	3	US-09-197-770B-12	Sequence 12, Appl
29	38	64.4	23	6	5426100-6	Patent No. 5426100
30	38	64.4	23	6	5426100-6	Patent No. 5426100
31	38	64.4	51	2	US-08-799-173A-11	Sequence 11, Appl
32	38	64.4	51	4	US-09-170-042A-11	Sequence 12, Appl
33	38	64.4	60	1	US-07-646-531D-12	Sequence 12, Appl
34	38	64.4	60	2	US-08-488-273-12	Patent No. 5426100
35	38	64.4	60	6	5426100-12	Patent No. 5426100
36	38	64.4	60	6	5426100-12	Sequence 14, Appl
37	38	64.4	568	1	US-07-862-021B-14	Sequence 14, Appl
38	38	64.4	568	5	PCT-US93-03164-14	Sequence 14, Appl
39	38	64.4	787	4	US-09-825-294-207	Sequence 207, App
40	38	64.4	787	4	US-09-970-966-207	Sequence 207, App
41	38	64.4	788	2	US-08-918-914-4	Sequence 4, Appl
42	38	64.4	802	1	US-07-862-021B-12	Sequence 12, Appl
43	38	64.4	802	1	US-08-313-288B-12	Sequence 12, Appl
44	38	64.4	802	5	PCT-US93-03164-12	Sequence 12, Appl
45	38	64.4	807	1	US-07-862-021B-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-07-646-531D-5
; Sequence 5, Application US/07646531D
; Patent No. 5200397
; GENERAL INFORMATION:
; APPLICANT: Deutch, Alan Howard
; APPLICANT: Tuszyński, George Paul
; TITLE OF INVENTION: Peptide Fragments and Analogs of
; TITLE OF INVENTION: Thrombospondin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: W. R. Grace & Co. -Conn.
; STREET: 7379 Route 32
; CITY: Columbia
; STATE: Maryland
; COUNTRY: USA
; ZIP: 21044
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/646,531D
; FILING DATE: 19910131
; ATTORNEY/AGENT INFORMATION:
; NAME: Appleby, Vanessa L.
; REGISTRATION NUMBER: 33223
; REFERENCE/DOCKET NUMBER: 01-7896
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 531-4515
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-646-531D-5

Query Match 67.8%; Score 40; DB 1; Length 23;
Best Local Similarity 50.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSCXXCG 17

Db 4 WSEWTSCSTSCG 15

RESULT 2

US-08-488-273-5

Sequence 5, Application US/08488273
Patent No. 5840692
GENERAL INFORMATION:
APPLICANT: Deutch, Alan H.
APPLICANT: Tuszyński, George P.
TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
TITLE OF INVENTION: THROMBOSPONDIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/488,273
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/359,263
FILING DATE: 19-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,146
FILING DATE: 20-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,527
FILING DATE: 09-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/483,527
FILING DATE: 22-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-204
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
TELEFAX: (215) 567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-273-5

Query Match 67.8%; Score 40; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXXCSXCG 17
Db 4 WSEWTSCSTSCG 15

RESULT 3
US-09-197-770B-11
Sequence 11, Application US/09197770B
Patent No. 6339062
GENERAL INFORMATION:
APPLICANT: Tuszyński, George
APPLICANT: Williams, Taffy
APPLICANT: Actor, Paul
TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT
TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY
FILE REFERENCE: 07206-0021

QY 6 WSXXXCSXKCG 17
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Db 4 WSEWTSCTSCG 15

RESULT 6

US-08-985-526-1
; Sequence 1, Application US/08985526
; Patent No. 6080728

GENERAL INFORMATION:

; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/985,526

; FILING DATE:

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845

; FILING DATE: 16-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: McMorris Jr., Robert G

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 658-9141

; TELEFAX: (302) 658-5613

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-985-526-1

Query Match 67.8%; Score 40; DB 3; Length 218;

Best Local Similarity 50.0%; Pred. No. 29;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXKCG 17

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Db 85 WSEWTSCTSCG 96

RESULT 7

PCT-US93-01652-1

; Sequence 1, Application PC/TUS9301652

GENERAL INFORMATION:

; APPLICANT: Bouck, Noel P.

; APPLICANT: Polverini, Peter J.

; APPLICANT: Good, Deborah J.

; APPLICANT: Frazier, William A.

; TITLE OF INVENTION: Method and Composition for

; TITLE OF INVENTION: Inhibiting Angiogenesis

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut

; STREET: 100 South Wacker Drive, Suite 960

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-4002

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01652
; FILING DATE: 19930222

CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/841,656

; FILING DATE: 24-FEB-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/464,369

; FILING DATE: 12-JAN-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Pentress, Susan B.

; REGISTRATION NUMBER: 31,327

; REFERENCE/DOCKET NUMBER: 92005-PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312)-456-8000

; TELEFAX: (312)-456-7776

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 239 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

PCT-US93-01652-1

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Best Local Similarity 50.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXKCG 17

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Db 74 WSEWTSCTSCG 85

RESULT 8

US-08-985-526-3

; Sequence 3, Application US/08985526

; Patent No. 6080728

GENERAL INFORMATION:

; APPLICANT: Mixson, James A

; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA

; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE

; TITLE OF INVENTION: THERAPY

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Connolly, Bove, Lodge, & Hutz

; STREET: 1220 Market Street, P.O. Box 2207

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: U.S.A.

; ZIP: 19899

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/985,526

; FILING DATE:

CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/608,845

; FILING DATE: 16-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: McMorris Jr., Robert G

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 658-9141

TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-3

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Best Local Similarity 50.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXXCG 17
Db 85 WSEWTSCTSCG 96

RESULT 9
US-09-854-845-16
; Sequence 16, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 939
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-16

Query Match 67.8%; Score 40; DB 4; Length 939;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXXCG 17
Db 473 WSSWALCSTSCG 484

RESULT 10
US-09-854-845-14
; Sequence 14, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 954
; TYPE: PRT

; ORGANISM: homo sapiens
US-09-854-845-14

Query Match 67.8%; Score 40; DB 4; Length 954;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXXCG 17
Db 473 WSSWALCSTSCG 484

RESULT 11
US-09-854-845-6
; Sequence 6, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1034
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-6

Query Match 67.8%; Score 40; DB 4; Length 1034;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXXCG 17
Db 568 WSSWALCSTSCG 579

RESULT 12
US-09-854-845-2
; Sequence 2, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-2

Query Match 67.8%; Score 40; DB 4; Length 1049;
Best Local Similarity 50.0%; Pred. No. 94;

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(without alignments)
55.424 Million cell updates/sec

Title: US-09-462-909D-9
Perfect score: 59
Sequence: 1 XXXXXWSXXXCXCGXXXXX 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04:
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	67.8	23	2 AAR13629	Aar13629 Thrombosop
2	40	67.8	23	2 AAW81482	Aaw81482 Thrombosop
3	40	67.8	23	5 AAE20746	Aae20746 Thrombosop
4	40	67.8	23	8 ADM80537	Adm80537 Thrombosop
5	40	67.8	50	2 AAY49503	Aay49503 Human MET
6	40	67.8	50	4 AAB50005	Aab50005 TSP1 doma
7	40	67.8	143	4 ABB11084	Abb11084 Human sec
8	40	67.8	157	3 AAB08133	Aab08133 Amino aci
9	40	67.8	170	8 ADL70644	Adl70644 Human thr
10	40	67.8	183	5 AAU74791	Aau74791 Human thr
11	40	67.8	218	2 AAU40287	Aau40287 Human TSP
12	40	67.8	218	2 AAY06182	Aay06182 Thrombosop
13	40	67.8	239	2 AAR40823	Aar40823 Human thr
14	40	67.8	324	8 ADP04871	Adp04871 Sea squir
15	40	67.8	397	8 ADJ34131	Adj34131 Human sec
16	40	67.8	401	7 ADD18225	Add18225 Human mol
17	40	67.8	401	7 ADD18230	Add18230 Human mol
18	40	67.8	401	7 ADD18228	Add18228 Human mol
19	40	67.8	401	7 ADD18232	Add18232 Human mol
20	40	67.8	401	8 ADJ34125	Adj34125 Human sec
21	40	67.8	401	8 ADJ34123	Adj34123 Human sec
22	40	67.8	401	8 ADJ34121	Adj34121 Human sec
23	40	67.8	401	8 ADJ34127	Adj34127 Human sec
24	40	67.8	432	8 ADQ39359	Adq39359 Human myo
25	40	67.8	432	8 ADQ39357	Adq39357 Human myo

26	40	67.8	441	2 AAM40288	Aaw40288 Human con
27	40	67.8	441	2 AAY06183	Aay06183 Thrombosop
28	40	67.8	459	4 AAU02916	Aau02916 Angiotens
29	40	67.8	466	3 AAB43602	Aab43602 Human can
30	40	67.8	546	4 AAU02915	Aau02915 Angiotens
31	40	67.8	548	7 ADN02474	Adn02474 TSP polyp
32	40	67.8	555	4 AAU02914	Aau02914 Angiotens
33	40	67.8	606	5 ABG94994	Abg94994 Babesia a
34	40	67.8	606	8 ADP04709	Adp04709 Sea squir
35	40	67.8	731	4 AAU02913	Aau02913 Angiotens
36	40	67.8	939	5 AAG68296	Aag68296 Human sem
37	40	67.8	954	5 AAG68295	Aag68295 Human sem
38	40	67.8	999	3 AAY94990	Aay94990 Human sec
39	40	67.8	1034	5 AAG68291	Aag68291 Human sem
40	40	67.8	1049	5 AAG68289	Aag68289 Human sem
41	40	67.8	1078	5 AAG68292	Aag68292 Human sem
42	40	67.8	1092	5 ABG34077	Abg34077 Human PRO
43	40	67.8	1092	6 ADA01364	Ada01364 Human PRO
44	40	67.8	1092	6 ADA43793	Ada43793 Human sec
45	40	67.8	1092	6 ADA43561	Ada43561 Human sec

ALIGNMENTS

RESULT 1
AAR13629
ID AAR13629 standard; peptide; 23 AA.
XX AAR13629;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-1991 (first entry)
XX
DE Thrombospondin peptide p11.
XX
KW Antiviral agent; wound healing; platelet aggregation; thrombotic;
KW thrombolytic.
XX
OS Synthetic.
XX
PN EP443404-A.
XX
PD 28-AUG-1991.
XX
PF 11-FEB-1991; 91EP-00101908.
XX
PR 22-FEB-1990; 90US-00483527.
PR 31-JAN-1991; 91US-00646531.
(GRAC) GRACE & CO-CONN W R.
(MEDI-) MED COLLEGE OF PENNSYLVIA.
(DEUT/) DEUTCH A H.
PI Deutch AH, Tuszyński GP;
WPI; 1991-254044/35.
XX
DR New peptide fragments and analogues of thrombospondin - useful for
inhibiting tumour metastasis, as clotting agents and to promote or
inhibit cell adhesion and immune modulation.
XX
PS Claim 3; Page 26; 30pp; English.
XX
CC The peptide is a synthetic fragment of human thrombospondin and is based
on the sequence motif of Robson et al (Nature (1988) 335:79- 82). It has
thrombospondin-like activity and can be used: (1) to inhibit tumour cell
metastasis and atherosclerosis; (2) to promote or inhibit platelet
aggregation, angiogenic activity, thrombotic or thrombolytic activity,
(3) to promote wound healing, and (4)
as an antiviral agent (interferes with cell adhesion). The peptide is
prepd. by std. synthesis techniques. See also AAR13626-R13641. (Updated
on 25-MAR-2003 to correct PA field.)

u8-09-462-909d-9.rag

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[illegible]

Query Match 67.8%; Score 40; DB 5; Length 23;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 6; Indels 6; Gaps 0;

QY 6 WSXXXCSXXCG 17
 DB 4 WSEWTSCTSCG 15

RESULT 4
 ADM80537
 ID ADM80537 standard; peptide; 23 AA.
 XX AC
 XX ADM80537;
 XX DT 03-JUN-2004 (first entry)
 XX DE Thrombospondin analogue peptide #11.
 XX KW thrombospondin; tumour cell metastasis; cell invasion; cell adhesion;
 XX KW wound healing; implant acceptance; malaria; atherosclerosis; thrombosis.
 XX OS Synthetic.
 XX PN US2003171298-A1.
 XX PD 11-SEP-2003.
 XX PP 03-OCT-2001; 2001US-00042696.
 XX PR 23-NOV-1998; 98US-00197770.
 XX PX (INKI-) INKINE PHARM MCP HAHNEMANN.
 XX PY Williams T, Tuszyński G, Actor P;
 XX DR WPI; 2004-119157/12.
 XX PT New retroinverso polypeptide, useful for inhibiting tumor cell
 PT metastasis, invasion or adhesion, for promoting wound healing or implant
 PT acceptance, or for treating malaria, atherosclerosis or thrombosis.
 XX PS Claim 1; SEQ ID NO 11; Sipp; English.
 XX PX The invention relates to a polypeptide which has the retroinverso form of
 CC a polypeptide which mimics or inhibits the biological activity of
 CC thrombospondin. Also described is a method for inhibiting cell
 CC metastasis, invasion or adhesion, comprising administering to a host the
 CC retroinverso polypeptide compound. The retroinverso polypeptide is useful
 CC for inhibiting tumour cell metastasis, invasion or adhesion, for
 CC promoting wound healing or implant acceptance, or for treating malaria,
 CC atherosclerosis or thrombosis. The present sequence represents a
 CC thrombospondin analogue of the invention.

Query Match 67.8%; Score 40; DB 8; Length 23;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 6; Indels 6; Gaps 0;

QY 6 WSXXXCSXXCG 17
 DB 4 WSEWTSCTSCG 15

RESULT 5
 AAY49503
 ID AAY49503 standard; protein; 50 AA.
 XX AC
 XX AAY49503;
 XX DT 10-JAN-2000 (first entry)
 XX KW Human; METH; metalloprotease; thrombospondin; angiogenesis inhibition;

DE Human METH1 thombospondin-like domain #1.
 XX Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin;
 KW cancer; diagnosis; hyperproliferative disorder; autoimmune disease;
 KW angiogenesis inhibitor; abnormal wound healing; inflammation;
 KW rheumatoid arthritis; psoriasis; endometrial bleeding disorder;
 KW diabetic retinopathy; macula degeneration; haemangioma; detection;
 KW arterial-venous malformation; immune deficiency.
 XX OS Homo sapiens.
 XX PN WO9937660-A1.
 XX PD 29-JUL-1999.
 XX PF 22-JAN-1999; 99WO-US001313.
 XX PR 23-JAN-1998; 98US-0072298P.
 XX PR 28-AUG-1998; 98US-0098539P.
 XX PA (IRUE/) IRUELA-ARISPE L.
 XX PA (HAST/) HASTINGS G A.
 XX PA (RUBE/) RUBEN S M.
 XX PI IrueLA-Arispe L, Hastings GA, Ruben SM;
 XX WPI; 1999-590684/50.
 XX DR New isolated metalloprotease thrombospondin polypeptides, useful for
 PT treating hyperproliferative disorders, cancers or autoimmune disorders.
 XX PS Disclosure; Fig 5; 457pp; English.
 XX CC AA232000 and AA232001 encode, and AAY49501 and AAY49502 represent, human
 CC metalloprotease thrombospondin (METH) proteins METH1 and METH2
 CC respectively. METH1 and METH2 have been found to be potent inhibitors of
 CC angiogenesis both in vitro and in vivo. They can be used for treating
 CC cancer and other disorders related to angiogenesis including abnormal
 CC wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial
 CC bleeding disorders, diabetic retinopathy, some forms of macula
 CC degeneration, haemangiomas, and arterial-venous malformations. They may
 CC be useful in treating deficiencies or disorders of the immune system, by
 CC activating or inhibiting the proliferation, differentiation, or
 CC mobilisation (chemotaxis) of immune cells. The etiology of these immune
 CC deficiencies or disorders may be genetic, somatic, such as cancer or some
 CC autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or some
 CC infectious. They can also be used to treat inflammatory conditions, both
 CC chronic and acute conditions. The products can also be used for detection
 CC and diagnosis. AA232002 to AA232080, and AAY49503 to AAY49511 represent
 CC sequences given in the exemplification of the present invention

Query Match 67.8%; Score 40; DB 2; Length 50;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 6; Indels 6; Gaps 0;

QY 6 WSXXXCSXXCG 17
 DB 7 WSEWTSCTSCG 18

RESULT 6
 AAB50005
 ID AAB50005 standard; protein; 50 AA.
 XX AC
 XX AAB50005;
 XX DT 19-MAR-2001 (first entry)
 XX DE TSPI domain #1.
 XX KW Human; METH; metalloprotease; thrombospondin; angiogenesis inhibition;

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cancer therapy; benign tumour; ocular angiogenic disease;
 rheumatoid arthritis; psoriasis; wound healing; endometriosis;
 vasculogenesis; granulation; hypertrophic scar; nonunion fracture;
 scleroderma, trachoma; vascular adhesion; myocardial angiogenesis;
 coronary collateral; cerebral collateral; arteriovenous malformation;
 ischaemic limb angiogenesis; Osler-Webber syndrome; TSP domain;
 plaque neovascularisation; telangiectasia; haemophilic joint;
 angiofibroma; fibromuscular dysplasia; wound granulation;
 Crohn's disease; atherosclerosis; birth control.

Homo sapiens.

WO2000071577-A1.

30-NOV-2000.

25-MAY-2000; 2000WO-US014462.

25-MAY-1999; 99US-00318208.

20-JUL-1999; 99US-0144882P.

10-AUG-1999; 99US-0147823P.

13-AUG-1999; 99US-00373658.

22-DEC-1999; 99US-0171503P.

22-FEB-2000; 2000US-0183792P.

(HUMA-) HUMAN GENOME SCI INC.

(SMIK) SMITHKLINE BEECHAM CORP.

(BETH) BETH ISRAEL DEACONESS MEDICAL CENT.

(IRUE) IRUELA-ARISPE L.

(HAST) HASTINGS G A.

(RUBS) RUBEN S M.

(JONAK) JONAK Z L.

(TRUL) TRULLI S H.

(FORN) FORNWALD J A.

(TERR) TERRETT J A.

IrueLA-Arispe L, Hastings GA, Ruben SM, Jonak ZL, Trulli SH;
 Fornwald JA, Terrett JA;
 WPI; 2001-025136/03.

METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit
 angiogenesis in the treatment of disorders such as cancer, rheumatoid
 arthritis and psoriasis.

Disclosure; Fig 5; 768pp; English.

The present invention relates to human METH1 and METH2. (ME for
 metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003).
 The present sequence is a TSP domain which are found in METH protein.
 METH can be used for inhibiting angiogenesis in an individual, and for
 treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid
 arthritis, psoriasis, delayed wound healing, endometriosis,
 vasculogenesis, granulations, hypertrophic scars, nonunion fractures,
 scleroderma, trachoma, vascular adhesions, myocardial angiogenesis,
 coronary collaterals, cerebral collaterals, arteriovenous malformations,
 ischaemic limb angiogenesis, Osler-Webber syndrome, plaque
 neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 fibromuscular dysplasia, wound granulation, Crohn's disease or
 atherosclerosis. METH can also be used in birth control. METH can also be
 used in diagnostic methods for the prognosis of cancer

Sequence 50 AA;

Query Match 67.8%; Score 40; DB 4; Length 50;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WXXXXXCSXXCG 17
 |||||
 Db 7 WSEWTSCSTSCG 18

RESULT 7
 ABB11084
 ID ABB11084 standard; peptide; 143 AA.
 XX ABB11084;
 AC ABB11084;
 DT 11-JAN-2002 (first entry)
 XX Human secreted protein homologue, SEQ ID NO:1454.
 DE
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytosstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer.
 XX
 OS Homo sapiens.
 XX WO200157188-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 05-FEB-2001; 2001WO-US003800.
 PF
 XX 03-FEB-2000; 2000US-00496914.
 PR
 XX 27-APR-2000; 2000US-00560875.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI; 2001-457740/49.
 XX N-PSDB; ABA08328.
 DR
 XX Human proteins and DNA encoding sequences useful for preventing, treating
 PT angiogenesis in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 PS Claim 20; Page 144; 1963pp; English.
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth factor activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g. by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention

XX SQ Sequence 143 AA;

Query Match 67.8%; Score 40; DB 4; Length 143;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 6 WXXXXXXCSXXCG 17
||| |||
Db 89 WSSWALCSTSCG 100

RESULT 8
AAB08133
ID AAB08133 standard; protein; 157 AA.
AC AAB08133;
XX
DT 04-DEC-2000 (first entry)
XX
DE Amino acid sequence of hTSP-1 Type I repeat peptide (TRP).
XX
KW Type I repeat; thrombospondin-1; TSP-1; Type I repeat peptide; TRP; KIAA0688; KIAA0550; angiogenesis inhibitory protein; angiogenesis;
KW cancer; tumor; rheumatoid arthritis; psoriasis; retinopathy;
KW ocular angiogenic disease; macular degeneration; corneal graft rejection;
KW neovascular glaucoma; retrolental fibroplasia; rubeosis;
KW Osler-Webber Syndrome; myocardial angiogenesis; haemophilic joint;
KW plaque neovascularisation; telangiectasia; angiofibroma;
KW wound granulation; coronary collateral; cerebral collateral;
KW arteriovenous malformation; ischemic limb angiogenesis;
KW neovascular glaucoma; retrolental fibroplasia; fracture; vasculogenesis;
KW heliobacter related disease; hematopoiesis; ovulation; menstruation;
KW placenta; birth control; embryo implantation.
XX
OS Homo sapiens.
XX WO200047622-A2.
XX
PN 17-AUG-2000.
XX
PD
XX
PF 15-FEB-2000; 2000WO-GB000520.
XX
PR 15-FEB-1999; 99GB-00003408.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Mazarakis N, Martin-Rendon E, Kingsman SM;
XX WPI; 2000-549137/50.
XX
XX Non-naturally occurring Type I repeat peptide (TRP) derived from human thrombospondin-1, KIAA0688 or KIAA0550 proteins, useful in the treatment of angiogenesis and/or cancer.
XX
XX Claim 4; Fig 2; 84pp; English.
XX
XX The present sequence represents the amino acid of human thrombospondin-1 (hTSP-1) Type I repeat peptide (TRP). The specification describes a non-naturally occurring TRP, derived from hTSP-1, KIAA0688 or KIAA0550 proteins. The TRP protein is an angiogenesis inhibitory protein. TRP

CC proteins are used for the treatment of conditions associated with angiogenesis and cancer. Angiogenic mediated diseases include tumours, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, retinopathy of prematurity, macular degeneration, corneal graft rejection.

CC Neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilic joints, angiofibroma, wound granulation, coronary collaterals, cerebral collateral, arteriovenous malformations, ischemic limb angiogenesis, neovascular glaucoma, retrolental fibroplasia, heliobacter related diseases, fractures, vasculogenesis, hematopoiesis, ovulation, menstruation and placenta. TRPs are also useful in the treatment of disease of excessive or abnormal stimulation of endothelial cells. TRP can also be used as a birth control agent, as it prevents the vascularisation required for embryo implantation

XX SQ Sequence 157 AA;

Query Match 67.8%; Score 40; DB 3; Length 157;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 6 WXXXXXXCSXXCG 17
||| |||
Db 6 WSEWTSCTSCG 17

RESULT 9
ADL70644
ID ADL70644 standard; protein; 170 AA.
XX
AC ADL70644;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human thrombospondin-1 domain of type 1 repeats.
XX
KW Human; thrombospondin-1; epitope; cancer; diagnosis.
XX
OS Homo sapiens.
XX WO2004018995-A2.
XX
PN 04-MAR-2004.
XX
PD
XX
PF 20-AUG-2003; 2003WO-US026023.
XX
PR 23-AUG-2002; 2002US-0405494P.
XX 21-APR-2003; 2003US-00419462.
XX
XX (WILL/) WILLIAMS K J.
XX
XX Williams KJ;
XX
XX WPI; 2004-226901/21.
XX
XX
XX New purified thrombospondin fragment extracted from a body fluid, useful for diagnosing cancer e.g. adenoma, adenocarcinoma, carcinoma, lymphoma or leukemia or as calibrators, indicators, immunogens and analytes.
XX
XX Disclosure; SEQ ID NO 43; 76pp; English.
XX
XX The present sequence is that of the domain of type I repeats of human thrombospondin-1 (TSP) ADL70639, consisting of 3 type I repeats. It includes the C-terminal portion of the collagen V binding region; the remainder of this region lies in the procollagen homology domain CC ADL70643. The invention relates to TSP fragments (80-100, 40-55 or 20-35 kDa mol.wt.) found in plasma, and their use in clinical assays for cancer CC and for generation of antibodies and other binding agents. A method that CC distinguishes TSP from a TSP fragment or portion involves: (1) using an CC epitope shared by TSP and the TSP fragment or portion as a target for a CC binding molecule, e.g. an antibody, to obtain a quantitation of TSP plus CC TSP fragment or portion; (2) using an epitope present in TSP but not in CC the fragment or portion to obtain a quantitation of TSP only; and (3)

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using the difference between (1) and (2) as a quantitation of the amount of TSP fragment or portion. Suitable epitopes are provided ADL70602-ADL70638. Detection or quantification of the TSP fragment or portion is performed in order to detect the presence, or monitor the course, of a disease or condition selected from cancer, renal failure, renal disease, atopic dermatitis, vasculitis, acute vasculitis, renal allograft, asthma, diabetes mellitus, myocardial infarction, liver disease, splenectomy, dermatomyositis, polyarteritis nodosa, systemic lupus erythematosus, lupus erythematosus, Kawasaki syndrome, non-specific vasculitis, juvenile rheumatoid arthritis, rheumatoid arthritis, vasculitis syndrome, Henoch-Schoenlein purpura, thrombocytopenic purpura, purpura, an inflammatory condition, a condition associated with clotting, a condition associated with platelet activation, a condition associated with intravascular platelet activation, a condition associated with consumption of platelets, heparin-induced thrombocytopenia, disseminated intravascular coagulation, intravascular coagulation, extravascular coagulation, a condition associated with endothelial activation, a condition associated with production and/or release of thrombospondin and/or a thrombospondin fragment, urticaria, hives, angioedema, a drug reaction, an antibiotic reaction, an aspartame reaction, atopic dermatitis, eczema, hypersensitivity, scleroderma, conditions associated with plugging of vessels, a condition associated with a cryoglobulin, a condition associated with a cryoglobulin, and a condition associated with an anti-adenocarcinoma, carcinoma, lymphoma, leukaemia, solid cancer, liquid cancer, metastatic cancer, pre-metastatic cancer, non-metastatic cancer, a cancer with vascular invasion, internal cancer, skin cancer, cancer of the respiratory system, circulatory system, musculoskeletal system, muscle, bone, a joint, tendon or ligament, digestive system, liver or biliary system, pancreas, head, neck, endocrine system, reproductive system (male or female), genitourinary system, kidney, urinary tract, sensory system, nervous system, lymphoid organ, blood, a gland, mammary gland, prostate gland, endometrial tissue, mesodermal tissue, ectodermal tissue, endodermal tissue, a teratoma, a poorly-differentiated cancer, a well-differentiated cancer or a moderately differentiated cancer.

Sequence 170 AA;

Query Match 67.8%; Score 40; DB 8; Length 170;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
Db 7 WSEWTSCTSCG 18

RESULT 10
AAU74791
ID AAU74791 standard; protein; 183 AA.

XX AC AAU74791;

XX DT 09-APR-2002 (first entry)

XX DE Human thrombospondin-1 (TSP-1) derived recombinant protein, 3TSR.

XX KW Thrombospondin-1; TSP-1; cytostatic; angiogenesis; vasotropic; vulnary;
XX KW neovascularisation; cell proliferation inhibitor; cancer; solid tumour;
XX KW haemangioma; acoustic neuromas; neurofibroma; trachoma;
XX KW pyogenic granuloma; rheumatoid arthritis; ocular angiogenic disease;
XX KW retinopathy; psoriasis; macular degeneration; corneal graft rejection;
XX KW neovascular glaucoma; retrolental fibroplasia; rebeosis; angiofibroma;
XX KW Osler-Webber syndrome; myocardial angiogenesis; haemophilic joints;
XX KW plaque neovascularisation; telangiectasia; wound granulation; apoptosis;
XX KW mutant; mutein; 3TSR.

XX OS Homo sapiens.
XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Peptide 1.5
XX FT /label= Vector_derived_peptide

Protein 6. 175
/note= "Residues 361-530 of human thrombospondin-1 (TSP-1)"
Peptide 176. 183
/label= Vector_derived_peptide
XX WO200191781-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US017250.
XX 26-MAY-2000; 2000US-0207994P.
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX Lawler JW;
XX WPI; 2002-106273/14.
XX Composition useful for treatment of cancer comprises cDNA encoding amino acids of human thrombospondin-1 or its conservative variant and a carrier.
XX Example 1; Page; 54pp; English.
XX The invention describes a composition comprising cDNA encoding fragments of human thrombospondin-1 (TSP-1), a type 1 repeat polypeptide and a potent inhibitor of tumour growth and angiogenesis. The composition is useful for killing cancerous cells (preferably tumour); for reducing the volume or inhibiting growth of a tumour (inhibiting neovascularisation in the tumour); for decreasing proliferation of tumour cells; in the treatment of diseases and conditions associated with angiogenic activity or misregulated growth and angiogenesis-mediated diseases such as cancer, solid tumour, tumour metastasis, benign tumour, (e.g. haemangioma, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas), rheumatoid arthritis, psoriasis, ocular angiogenic diseases (e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rebeosis), Osler-Webber syndrome, myocardial angiogenesis, telangiectasia, plaque neovascularisation, haemophilic joints, angiofibroma or wound granulation. The composition induces apoptosis and inhibits neovascularisation in the tumour cells. This amino acid sequence represents a recombinant protein, 3TSR, derived from human thrombospondin-1 (TSP-1) and containing the 3 type 1 repeat (TSR) regions of TSP-1, described in the method of the invention. Note: This sequence does not appear in the specification but has been created using the human thrombospondin-1 (TSP-1) wild type sequence (see AAU74771) from information given in the invention

Query Match 67.8%; Score 40; DB 5; Length 183;

Best Local Similarity 50.0%; Pred. No. 54;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
Db 12 WSEWTSCTSCG 23

RESULT 11
AAW40287
ID AAW40287 standard; protein; 218 AA.

XX AC AAW40287;

XX DT 18-AUG-1998 (first entry)

XX DE Human TSP1 protein.

XX KW TSP1; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy;
XX KW liposome; DNA complex; tumour suppressor protein; treatment; neoplastic;


```

KW metabolic disease; tumour.
XX
OS Homo sapiens.
XX
FH Key
XX Location/Qualifiers
FT Peptide
XX 12..27
FT Peptide
XX /label= anti-angiogenic peptide
FT Peptide
XX 142..159
FT Misc-difference 160
XX /label= anti-angiogenic peptide
FT Peptide
XX /note= "encoded by CGG"
FT Peptide
XX 199..217
FT Misc-difference 217
XX /label= anti-angiogenic peptide
FT /note= "encoded by CT"
XX
PN EP819758-A2.
XX
XX
XX 21-JAN-1998.
XX
XX 16-JUL-1997; 97BP-00112154.
XX
XX 16-JUL-1996; 96US-00680845.
XX
XX (MIXS/) MIXSON A J.
XX
XX Mixson AJ;
XX
XX WPI; 1998-078839/08.
XX N-PSDB; AAV10493.
XX
XX Complexes of DNA encoding anti-angiogenic peptide - with cationic
XX liposome(s) or cationic polymer, useful for, e.g. gene therapy of
XX tumours.
XX
XX Claim 9; Page 6; 47pp; English.
XX
XX This sequence represents the thrombospondin gene TSP1 which is used in a
XX method to produce a cationic vehicle consisting of a cationic
XX liposome:DNA complex where the DNA encodes an anti-angiogenic peptide or
XX tumour suppressor protein. Such complexes are used for treatment of
XX neoplastic and metabolic diseases especially for gene therapy of tumours
XX
XX Sequence 218 AA;
XX
XX Query Match 67.8%; Score 40; DB 2; Length 218;
XX Best Local Similarity 50.0%; Pred. No. 62;
XX Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
QY 6 WXXXXXXCSXXCG 17
XX |||||
XX 85 WSEWTSCTSCG 96
XX
RESULT 12
AAAY06182
ID AAY06182 standard; protein; 218 AA.
XX
XX AC AAY06182;
XX
XX 16-AUG-1999 (first entry)
XX
XX Thrombospondin I fragment.
XX
XX Anti-angiogenic; carrier:DNA complex; tumour; gene therapy; human;
XX Thrombospondin I; melanoma; lung cancer; colon cancer; brain cancer;
XX breast cancer.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 160
XX /note= "encoded by CGG"
XX
FT

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FT Misc-difference 161
XX /note= "encoded by CTC"
FT Misc-difference 162
XX /note= "encoded by TGC"
FT Misc-difference 163
XX /note= "encoded by AAC"
FT Misc-difference 177
XX /note= "encoded by GAA"
FT Misc-difference 178
XX /note= "encoded by GCG"
FT Misc-difference 179
XX /note= "encoded by CGG"
XX
PN EP921193-A1.
XX
XX 09-JUN-1999.
XX
XX 07-JAN-1998; 98EP-00100135.
XX
XX 05-DEC-1997; 97US-00985526.
XX
XX (MIXS/) MIXSON A J.
XX
XX Mixson AJ;
XX
XX WPI; 1999-315406/27.
XX N-PSDB; AAX58725.
XX
XX Inhibition of growth of solid tumors.
XX
XX Disclosure; Page 17-18; 46pp; English.
XX
XX This sequence represents an anti-angiogenic fragment of the
XX thrombospondin I protein. The invention provides a carrier:DNA complex
XX that comprises DNA (see AAX58725-42) coding for an anti-angiogenic
XX protein or peptide, the complex being deliverable to the site of a tumour
XX in vivo, and which additionally comprises regulatory elements for
XX expressing the anti-angiogenic DNA in a tumour or tumour vasculature. The
XX complex may also include DNA encoding a tumour suppressor protein,
XX especially p53. The carrier is a liposome, cationic polymer, micelle,
XX microsphere, virus, viral component, or a combination of these, and
XX administration is by intravenous or intratumoral injection. The complexes
XX are useful in gene therapy for inhibition of tumour growth. The types of
XX tumors which may be treated include solid tumors such as melanomas and
XX tumors in the lung, colon, brain and breast
XX
XX Sequence 218 AA;
XX
XX Query Match 67.8%; Score 40; DB 2; Length 218;
XX Best Local Similarity 50.0%; Pred. No. 62;
XX Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
QY 6 WXXXXXXCSXXCG 17
XX |||||
XX 85 WSEWTSCTSCG 96
XX
RESULT 13
AAR40823
ID AAR40823 standard; protein; 239 AA.
XX
XX AC AAR40823;
XX
XX 25-MAR-2003 (revised)
XX 03-MAR-1994 (first entry)
XX
XX Human thrombospondin 1.
XX
XX hTSP-1; platelet glycoprotein; angiogenesis; neovascularisation;
XX inhibitor; solid tumour; skin cancer; angiogenic dysfunction; melanoma;
XX diabetic retinopathy; psoriasis; neovascular glaucoma; Kaposi's sarcoma;
XX inflammation; retrolental fibroplasia.
XX
XX

```

OS	Homo sapiens.
XX	
XX	WO9316716-A1.
PPN	
XX	
XX	02-SEP-1993.
PD	
XX	
XX	22-FEB-1993; 93WO-US001652.
PP	
XX	
XX	24-FEB-1992; 92US-00841656.
PPR	
XX	(NOUN) UNIV NORTHWESTERN.
XX	
XX	Bouck NP, Polverini PJ, Good DJ, Frazier WA;
PI	
XX	
XX	WPI; 1993-288118/36.
DR	
XX	
PT	Compens. for inhibiting angiogenesis - contg. a vascularisation inhibitor
XX	comprising a peptide capable of inhibiting vascularisation.
PT	
PT	
XX	Claim 10; Page 41-42; 51pp; English.
XX	
XX	Certain fragments of thrombospondin, a glycoprotein found in the alpha
CC	granules of platelets, can inhibit vascularisation. Peptides derived from
CC	the hTSP sequence are useful for inhibiting neovascularisation, esp. in
CC	solid tumours such as melanomas. The inhibitory peptides can also be used
CC	in other diseases involving angiogenic dysfunction. See AAR40824-R40830.
CC	(Updated on 25-MAR-2003 to correct FN field.)
CC	
XX	
XX	Semence 239 AA;
XX	

XX	Compen. for inhibiting angiogenesis - contg. a vascularisation inhibitor
XX	comprising a peptide capable of inhibiting vascularisation.
XX	
XX	Claim 10; Page 41-42; 51pp; English.
XX	
XX	Certain fragments of thrombospondin, a glycoprotein found in the alpha
XX	granules of platelets, can inhibit vascularisation. Peptides derived from
CC	the ntSP sequence are useful for inhibiting neovascularisation, esp. in
CC	solid tumours such as melanomas. The inhibitory peptides can also be used
CC	in other diseases involving angiogenic dysfunction. See AAR40824-R40830.
CC	(Updated on 25-MAR-2003 to correct FN field.)
XX	
XX	Sequence 239 AA;

Query Match	67.8%	Score 40;	DB 2;	Length 239;
Best Local Similarity	50.0%;	Pred. No. 67;		
Matches	6;	Conservative	0;	Mismatches 6;
Indels				0;
Gaps				0;

RESULT 14	
ADP04871	ADP04871 standard; protein; 324 AA.
ID	ADP04871 standard; protein; 324 AA.
XX	
XX	ADP04871;
XX	
XX	29-JUL-2004 (first entry)
XX	
XX	Sea squirt protein with tissue specific expression in development Seq466.
DE	
XX	sea squirt; regeneration medicine; gene therapy; cell proliferation;
XX	differentiation; reproduction; environmental measurement; water survey.
KW	
KW	
XX	
XX	Ciona intestinalis.
OS	
XX	
XX	JP2004057129-A.
PN	
XX	
XX	26-FEB-2004.
PD	
XX	
XX	31-JUL-2002; 2002JP-00222593.
PF	
XX	
XX	31-JUL-2002; 2002JP-00222593.
PR	
XX	
XX	(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA	
XX	
XX	WPI: 2004-287079/27.
DR	
DR	N-PSDB; ADP04870.
XX	
XX	Novel gene cluster which is specifically expressed in tissue or organ
PT	during developmental phase of sea squirt, useful for elucidation of
PT	mechanism of development of tissue or organ of sea squirt.
PT	
XX	
XX	Claim 1; SEQ ID NO 466; 1846pp; Japanese.
PS	
XX	
XX	

PI Eisen A, Ellerman K, Gerlach VL, Gorman L, Guo X, Gusev VY, Ji W;
PI Li L, Macdougall JR, Malyankar UM, Millet I, Ort T, Padigar M;
PI Prayaga SK, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PI Rothenberg ME, Sciore P, Shenoy SG, Smithson G, Spytek KA, Stone DJ;
PI Taupier RJ, Tchernev VT, Vernet CAM, Voss EZ, Zerhusen BD, Zhong M;
XX WPI; 2004-082483/08.
DR N-PSDB; ADJ34130.
DR XX
PT XX
PT PT
PT PT
PT XX
PT XX
PS Claim 1; SEQ ID NO 20; 418pp; English.
XX
CC The invention relates to a new isolated polypeptide (designated NOVX)
CC comprising one of 141 fully defined sequences, their mature forms, a
CC protein comprising one or more conservative substitutions or having at
CC least 95% identity to one of the 141 proteins. Also included are a
CC composition comprising NOVX (or a NOVX nucleic acid molecule (NA)), a kit
CC comprising the composition of NOVX in one or more containers, an isolated
CC nucleic acid molecule encoding a NOVX protein, producing NOVX (comprising
CC culturing a cell under conditions that lead to expression of the
CC polypeptide, where the cell comprises a vector comprising NOVX NA),
CC identifying an agent that binds to NOVX, identifying a potential
CC therapeutic agent for use in the treatment of a pathology that is related
CC to aberrant expression or physiological interactions of NOVX, screening
CC for a modulator of activity of or latency or predisposition to a
CC pathology associated with NOVX, modulating the activity of NOVX, treating
CC or preventing a pathology associated with NOVX, treating a pathological
CC state in a mammal, a vector comprising the NOVX nucleic acid molecule, a
CC cell comprising the vector, an antibody that immunospecifically binds to
CC NOVX, determining the presence or amount of NOVX or the nucleic acid
CC molecule in a sample, and determining the presence of or predisposition
CC to a disease associated with altered levels of expression of NOVX or the
CC nucleic acid molecule in a first mammalian subject. The methods and
CC compositions of the present invention are useful for the diagnosis and
CC treatment of disorders associated with aberrant expression or activity of
CC the NOVX polypeptide, such as cancer, diabetes, obesity, and endocrine,
CC CNS and inflammatory disorders. They can also be used in various
CC detection and screening assays, chromosome mapping, tissue typing, gene
CC therapy and predictive medicine. The present sequence represents a NOVX
CC protein.
XX
SQ Sequence 397 AA;
Query Match 67.8%; Score 40; DB 8; Length 397;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 WXXXXXCSXXCG 17
DB 58 WSSWALCSTSCG 69
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Job time : 154.522 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:24:31 ; Search time 75.6522 Seconds
(without alignments)
81.226 Million cell updates/sec

Title: US-09-462-909D-8
Perfect score: 77
Sequence: 1 WSGWSSCSRSCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	77	100.0	867	1	SSPO_BOVIN	P98167 bos taurus
2	77	100.0	5146	2	Q8SPM4	Q8SPM4 bos taurus
3	73	94.8	4998	2	Q8C665	Q8C665 mus musculus
4	73	94.8	5141	2	Q700K0	Q700K0 rattus norv
5	70	90.9	880	2	Q8MSF8	Q8MSF8 drosophila
6	70	90.9	880	2	Q9VKV3	Q9VKV3 drosophila
7	67	87.0	168	2	Q9GZ21	Q9GZ21 cryptospori
8	67	87.0	1088	2	Q6PCK8	Q6PCK8 xenopus lae
9	67	87.0	1361	2	Q6PD18	Q6PD18 mus musculus
10	67	87.0	1461	2	Q8MYA8	Q8MYA8 caenorhabdi
11	67	87.0	1641	2	Q68SA9	Q68SA9 mus musculus
12	66	85.7	1637	2	Q9XSV8	Q9XSV8 bos taurus
13	65	84.4	125	2	Q72292	Q72292 caenorhabdi
14	65	84.4	238	2	Q76510	Q76510 cryptospori
15	65	84.4	685	2	Q9TTS5	Q9TTS5 bos taurus
16	65	84.4	769	2	Q8WEL5	Q8WEL5 drosophila
17	65	84.4	975	2	Q7Z291	Q7Z291 caenorhabdi
18	65	84.4	998	2	Q7PWY7	Q7PWY7 anopheles g
19	65	84.4	987	1	AT57 HUMAN	Q9UKP4 homo sapien
20	65	84.4	1020	2	Q19204	Q19204 caenorhabdi
21	65	84.4	1020	2	Q8IU50	Q8IU50 caenorhabdi
22	65	84.4	1059	2	Q9W493	Q9W493 drosophila
23	65	84.4	1886	2	Q6P7J9	Q6P7J9 homo sapien
24	65	84.4	3869	2	Q86PQ3	Q86PQ3 cryptospori
25	64	83.1	257	2	Q966K7	Q966K7 caenorhabdi
26	64	83.1	1089	2	Q8T3A0	Q8T3A0 ciona intes
27	64	83.1	2098	2	Q25757	Q25757 plasmodium
28	64	83.1	2114	2	Q97267	Q97267 plasmodium
29	63	81.8	415	2	O44228	O44228 halocynthia
30	63	81.8	1210	1	AT19 MOUSE	P59509 mus musculus
31	63	81.8	1224	1	AT16_HUMAN	Q8TE57 homo sapien

32 63 81.8 1502 2 Q9UPZ6 Q9UPZ6 homo sapien
33 63 81.8 1668 2 Q69ZU6 Q69ZU6 mus musculus
34 63 81.8 2401 2 Q7RF52 Q7RF52 plasmodium
35 62 80.5 504 2 Q69HL7 Q69HL7 ciona intes
36 62 80.5 808 2 O42113 O42113 brachydanio
37 62 80.5 1081 1 AT18_HUMAN AT18_HUMAN
38 62 80.5 1092 2 Q8BKA1 Q8BKA1 mus musculus
39 62 80.5 1221 2 Q6P4R5 Q6P4R5 homo sapien
40 61 79.2 129 2 Q8IVU0 Q8IVU0 homo sapien
41 61 79.2 551 1 YVD3 CAEEL YVD3 CAEEL
42 61 79.2 803 2 O42114 O42114 brachydanio
43 61 79.2 872 2 Q22580 Q22580 caenorhabdi
44 61 79.2 900 2 Q8K206 Q8K206 mus musculus
45 61 79.2 1009 2 Q8BKY1 Q8BKY1 m mus muscu

ALIGNMENTS

RESULT 1
ID SSPO_BOVIN STANDARD; PRT; 867 AA.
AC P98167;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE SCO-spondin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endomycyte;
RX MEDLINE=96338614; PubMed=8743952;
RA Gobron S., Monnerie H., Meinzel R., Creveaux I., Lehmann W.,
RA Lamalle D., Dastugue B., Meinzel A.;
RA "SCO-spondin: A new member of the thrombospondin family secreted by
RT the subcommissural organ is a candidate in the modulation of neuronal
RT aggregation.";
RL J. Cell Sci. 109:1053-1061(1996).
CC -!- FUNCTION: Involved in the modulation of neuronal aggregation.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Subcommissural organ.
CC -!- DEVELOPMENTAL STAGE: Embryo.
CC -!- SIMILARITY: Belongs to the thrombospondin family.
CC -!- SIMILARITY: Contains at least 2 EGF-like domains.
CC -!- SIMILARITY: Contains at least 1 F5/8 type C domain.
CC -!- SIMILARITY: Contains at least 3 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains at least 4 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 VWFC domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC HSPB; X93922; CAA63815.1; -.
CC HSPB; P01130; 1AJU.
CC InterPro; IPR002919; Cysrich_TIL.
CC InterPro; IPR000421; FAS8.C.
CC InterPro; IPR008979; Gal_Bind-like.
CC InterPro; IPR002172; LDL_receptor_A.
CC InterPro; IPR009041; PMP_SGCI.
CC InterPro; IPR000894; TSP1.
CC InterPro; IPR008085; TSP1.
CC InterPro; IPR001007; VWFC.
CC Pfam; PF00754; F5_F8_type_C; 1.
CC Pfam; PF00057; Ldl_recept_a; 3.

DR Pfam; PF01826; TIL; 1.
 DR Pfam; PF00090; TSP_1; 4.
 DR Pfam; PF00093; VWC_1.
 DR PRINTS; PRO0261; LDLRECEPTOR.
 DR PRINTS; PRO1705; TSP1REPEAT.
 DR PROSITE; PS01285; FA58C_1; 1.
 DR PROSITE; PS01286; FA58C_2; 1.
 DR PROSITE; PS50022; FA58C_3; 1.
 DR PROSITE; PS01209; LDLRA_1; 3.
 DR PROSITE; PS50068; LDLRA_2; 3.
 DR PROSITE; PS50092; TSP1; 4.
 DR PROSITE; PS50184; VWC_2; 1.
 KW Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein; Repeat.
 FT NON TER 1 87 TSP type-1 1.
 FT DOMAIN 29 142 EGF-like 1.
 FT DOMAIN 103 180 EGF-like 2.
 FT DOMAIN 143 244 TSP type-1 2.
 FT DOMAIN 245 304 VWC.
 FT DOMAIN 344 502 F5/8 type C.
 FT DOMAIN 506 544 LDL-receptor class A 1.
 FT DOMAIN 663 701 LDL-receptor class A 2.
 FT DOMAIN 723 761 LDL-receptor class A 3.
 FT DOMAIN 761 814 TSP type-1 3.
 FT DOMAIN 816 866 TSP type-1 4.
 FT DISULFID 107 122 By similarity.
 FT DISULFID 116 127 By similarity.
 FT DISULFID 129 141 By similarity.
 FT DISULFID 147 166 By similarity.
 FT DISULFID 149 169 By similarity.
 FT DISULFID 171 179 By similarity.
 FT DISULFID 344 502 By similarity.
 FT DISULFID 508 520 By similarity.
 FT DISULFID 515 533 By similarity.
 FT DISULFID 527 542 By similarity.
 FT DISULFID 665 677 By similarity.
 FT DISULFID 672 690 By similarity.
 FT DISULFID 684 699 By similarity.
 FT DISULFID 725 737 By similarity.
 FT DISULFID 732 750 By similarity.
 FT DISULFID 744 759 By similarity.
 FT CARBOHYD 88 88 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 409 409 N-linked (GlcNAc...) (potential).
 FT NON TER 867 867
 SQ SEQUENCE 867 AA; 91817 NW; 9538F2108E787B49 CRC64;
 Query Match 100.0%; Score 77; DB 1; Length 967;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WSGWSSCSRSCG 12
 Db 767 WSGWSSCSRSCG 778
 RESULT 2
 ID Q8SPM4 PRELIMINARY; PRT; 5146 AA.
 AC Q8SPM4;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE SCO-spondin.
 GN Name=sco-spondin;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Subcommisural organ;

RX MEDLINE=20465125; PubMed=11008217;
 RX DOI=10.1002/1098-1136(200011)32:2<177::AID-GLIA70>3.0.CO;2-V;
 RA Gobron S.;
 RT "Subcommisural organ/Reissner's fiber complex: characterization of
 RT SCO-spondin, a glycoprotein with potent activity on neurite
 RT outgrowth.";
 RL Glia 32:177-191(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Subcommisural organ;
 RA Meinzel A.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC 1- SIMILARITY: Contains 1 F5/8 type C domain.
 DR EMBL; AJ416457; CAC94914.1; --
 DR HSP; P98162; IK7B.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0030414; F:protease inhibitor activity; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR002919; Cysrich.TIL.
 DR InterPro; IPR006207; Cys_knot_C.
 DR InterPro; IPR011489; EMI.
 DR InterPro; IPR000421; FA58_C.
 DR InterPro; IPR001545; Gly hormoneB.
 DR InterPro; IPR002172; LDL receptor A.
 DR InterPro; IPR008037; Prot inh_PMP.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR001007; VWF_C.
 DR InterPro; IPR001846; VWF_D.
 DR Pfam; PF07546; EMI; 1.
 DR Pfam; PF00754; F5 F8 type C; 1.
 DR Pfam; PF00057; Ldl recept a; 10.
 DR Pfam; PF05375; Pacifastin_1; 1.
 DR Pfam; PF01826; TIL; 10.
 DR Pfam; PF00090; TSP_1; 25.
 DR Pfam; PF00093; VWC; 1.
 DR Pfam; PF00094; VWD; 3.
 DR PRINTS; PRO0261; LDLRECEPTOR.
 DR SMART; SM00041; CT; 1.
 DR SMART; SM00231; FA58C; 1.
 DR SMART; SM00068; GHB; 1.
 DR SMART; SM00192; LDLA; 10.
 DR SMART; SM00209; TSP1; 25.
 DR SMART; SM00214; VWC; 3.
 DR SMART; SM00216; VWD; 3.
 DR PROSITE; PS01225; CTCK 2; 1.
 DR PROSITE; PS01285; FA58C_1; UNKNOWN_1.
 DR PROSITE; PS01286; FA58C_2; 1.
 DR PROSITE; PS00022; FA58C_3; 1.
 DR PROSITE; PS00261; GLYCO HORMONE BETA_1; 2.
 DR PROSITE; PS01209; LDLRA_1; 7.
 DR PROSITE; PS00068; LDLRA_2; 9.
 DR PROSITE; PS50092; TSP1; 25.
 DR PROSITE; PS01208; VWF_C_1; UNKNOWN_1.
 DR PROSITE; PS0184; VWF_C_2; 2.
 DR PROSITE; PS0184; VWF_C_2; 2.
 SQ SEQUENCE 5146 AA; 543588 MW; 724C5FB8727E13DA CRC64;
 Query Match 100.0%; Score 77; DB 2; Length 5146;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WSGWSSCSRSCG 12
 Db 2485 WSGWSSCSRSCG 2496
 RESULT 3
 ID Q8CG65 PRELIMINARY; PRT; 4998 AA.
 AC Q8CG65;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE SCO-spondin.
GN Name=SCO-spondin; Synonyms=sco-spondin;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;
RA Goncalves N., Simon-Chazottes D., Creveaux I., Meinzel A.,
RT "Mouse SCO-spondin, a gene of the thrombospondin type 1 repeat (TSR)
superfamily expressed in the brain.";
RL Gene 312:263-270(2003).
CC -1- SIMILARITY: Contains 1 F5/8 type C domain.
DR EMBL; AJ491857; CAD42654.1; -.
DR HSSP; P01130; 1AJJ.
DR MGD; MGI:2674311; Sco-spondin.
DR GO; GO:0005737; Cytoplasm; IC.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR002919; Cys-rich_TIL.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011489; EMI.
DR InterPro; IPR000421; FAS8_C.
DR InterPro; IPR001545; Gly_hormoneB.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR008037; Pro_inh_PMP.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF07546; EMI; 1.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00057; Ldl_recept_a; 10.
DR Pfam; PF05375; Pacifastin_I; 1.
DR Pfam; PF01826; TIL; 10.
DR Pfam; PF00090; TSP_1; 25.
DR Pfam; PF00093; VWC_1.
DR Pfam; PF00094; VWD; 2.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00231; FAS8C; 1.
DR SMART; SM00068; GHb; 1.
DR SMART; SM00192; LDLa; 10.
DR SMART; SM00209; TSP1; 25.
DR SMART; SM00214; VWC; 4.
DR SMART; SM00216; VWD; 3.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS50022; FAS8C_3; 1.
DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS50068; LDLRA_2; 10.
DR PROSITE; PS50092; TSP1; 25.
DR PROSITE; PS01208; VWF_C; 1; UNKNOWN_1.
DR PROSITE; PS0184; VWF_C_2; 2.
SQ SEQUENCE 4998 AA; 535028 MW; DA2ABA8DA47DF225 CRC64;

Query Match 94.8%; Score 73; DB 2; Length 4998;
Best Local Similarity 91.7%; Pred. No. 0.2;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
Db 2342 WSGWSDCSRSCG 2353
||||| |||||

RESULT 4
Q700KO
ID Q700KO PRELIMINARY; PRT; 5141 AA.
AC Q700KO

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SCO-spondin.
GN Name=sco-spondin;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Meinzel O.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 F5/8 type C domain.
DR EMBL; AJ629845; CAF33425.1; -.
DR HSSP; P01130; 1AJJ.
DR GO; GO:0007155; P-cell adhesion; IEA.
DR InterPro; IPR002919; Cys-rich_TIL.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011489; EMI.
DR InterPro; IPR000421; FAS8_C.
DR InterPro; IPR001545; Gly_hormoneB.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR006552; VWF_C.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF07546; EMI; 1.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00057; Ldl_recept_a; 8.
DR Pfam; PF01826; TIL; 10.
DR Pfam; PF00090; TSP_1; 25.
DR Pfam; PF00093; VWC_1.
DR Pfam; PF00094; VWD; 3.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00192; LDLa; 10.
DR SMART; SM00209; TSP1; 25.
DR SMART; SM00214; VWC; 5.
DR SMART; SM00215; VWC_out; 9.
DR SMART; SM00216; VWD; 3.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS50022; FAS8C_3; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_2.
DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS50068; LDLRA_2; 10.
DR PROSITE; PS50092; TSP1; 24.
DR PROSITE; PS01208; VWF_C; 1; UNKNOWN_1.
DR PROSITE; PS50184; VWF_C_2; 2.
SQ SEQUENCE 5141 AA; 550644 MW; 1772AE67F02CA5E3 CRC64;

Query Match 94.8%; Score 73; DB 2; Length 5141;
Best Local Similarity 91.7%; Pred. No. 0.21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
Db 2491 WSGWSDCSRSCG 2502
||||| |||||

RESULT 5
Q8MSF8
ID Q8MSF8 PRELIMINARY; PRT; 880 AA.
AC Q8MSF8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GM15606P.
GN ORFNames=CG6232;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Fri Apr 1 15:03:06 2005

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OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AY118949; AAM50709.1; -
DR HSP; P07996; 1LSL.
DR FlyBase: FBgn0032252; CG6232.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00090; TSP_1; 3.
DR SMART; SM00209; TSP1; 6.
DR PROSITE; PS09000; PLAC; 1.
DR PROSITE; PS0092; TSP1; 5.
SQ SEQUENCE 880 AA; 98682 MW; FB3FA4D5B54106CE CRC64;
Query Match 90.9%; Score 70; DB 2; Length 880;
Best Local Similarity 91.7%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WSGWSSCSRSCG 12
Db 185 WSDWSSCSRSCG 196

RESULT 6
Q9VKV3 PRELIMINARY; PRT; 880 AA.
AC Q9VKV3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG6232-PA
GN ORFNames=CG6232;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RA MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

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Query Match      87.0%; Score 67; DB 2; Length 168;
Hit Local Similarity 83.3%; Prid. No. 0.07;
Species 10; Conservative 2; Indels 0; Gaps 0;

1 WSGWSSCSRSRSG 12
|||||
85 WSGWSDCSTSG 96

T J 8
S
Q6PCK8 PRELIMINARY; PRT; 1088 AA.
Q6PCK8;
05-JUL-2004 (TRENBLrel. 27, Created)
05-JUL-2004 (TRENBLrel. 27, Last sequence update)
05-JUL-2004 (TRENBLrel. 27, Last annotation update)
MGC68835 protein.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Reha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullhaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC058991; AAH58991.1; -
DR HSP; P15167; IATL.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR010909; PLAC_1.
DR InterPro; IPR008884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP 1; 6.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1; 7.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSP1; 6.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 1361 AA; 149549 MW; 49D04B6A28AFA877 CRC64;

Query Match 87.0%; Score 67; DB 2; Length 1361;
Best Local Similarity 83.3%; Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRCSCG 12
DB 277 WSAWSDCSRCSCG 288

RESULT 10
ID Q8MYA8 PRELIMINARY; PRT; 1461 AA.
AC Q8MYA8; Q17591; Q22300; (Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE ADT-1 (Hypothetical protein C02B4.1).
GN Name=adt-1; ORFName=C02B4.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuno K., Baba C., Asaka A., Hosono R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;

RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA McMurray A.A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB066246; BAC05514.1; -
DR EMBL; Z50004; CAA90293.2; -
DR EMBL; Z50006; CAA90293.2; JOINED.
DR EMBL; Z50004; CAA90302.2; JOINED.
DR EMBL; Z50006; CAA90302.2; -
DR HSP; F07996; ILSL.
DR MEROPS; M12.302; -
DR WormBase; WBGene0000082; adt-1.
DR WormPep; C02B4.1; CE31872.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR008884; TSP1.
DR InterPro; IPR008085; TSP 1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP 1; 12.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1; 13.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50092; TSP1; 12.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 1461 AA; 162615 MW; 3CFDC1C07C1F493A CRC64;

Query Match 87.0%; Score 67; DB 2; Length 1461;
Best Local Similarity 83.3%; Pred. No. 0.47;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRCSCG 12
DB 1088 WSDWSSCSRCSCG 1099

RESULT 11
ID Q68SA9 PRELIMINARY; PRT; 1641 AA.
AC Q68SA9;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE ADAMTS7B.
GN Name=Adamts7; (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15192113; DOI=10.1074/jbc.M402380200;
RA Somerville R.P.T., Longpre J.M., Apel E.D., Wang L.W.,
RA Sanes J.R., Leduc R., Apte S.S.;
RT "ADAMTS7B, the full-length product of the ADAMTS7 gene, is a
RT chondroitin sulfate proteoglycan containing a mucin domain.";
RL J. Biol. Chem. 279:35159-35175(2004).
DR EMBL; AY551090; AAT36307.1; -
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR008884; TSP1.
DR InterPro; IPR008085; TSP 1.
DR Pfam; PF05986; ADAM_spacer1; 1.

DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP 1; 6.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00209; TSP1; 8.
DR PROSITE; PS00215; ADAM_MEPPO; 1.
DR PROSITE; PS00092; TSP1; 6.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 1641 AA; 180743 MW; BA3B1E7B492D6165 CRC64;

Query Match 87.0%; Score 67; DB 2; Length 1641;
Best Local Similarity 83.3%; Pred. No. 0.52;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRS CG 12
DB 529 WSAWSDCSRS CG 540

RESULT 12
Q9XSV8 PRELIMINARY; PRT; 1637 AA.

AC Q9XSV8
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SCO-spondin (Fragment).
GN Name-sco-spondin;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Gobron S., Creveaux I., Didier R., Meinzel R.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133488; CAB46239.1; --
DR HSSP; P07996; ILSL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR001545; Gly_hormoneB.
DR InterPro; IPR009041; PMP_SGCI.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP 1.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01826; TIL; 3.
DR Pfam; PF00090; TSP 1; 11.
DR Pfam; PF00093; VWC_1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00041; CT; 1.
DR SMART; SM00068; GHF; 1.
DR SMART; SM00209; TSP1; 11.
DR SMART; SM00214; VWC; 2.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 2.
DR PROSITE; PS00092; TSP1; 11.
DR PROSITE; PS01208; VWF_C_1; UNKNOWN 1.
DR PROSITE; PS0184; VWF_C_2; 1.
FT NON_TER 1_1

SQ SEQUENCE 1637 AA; 173346 MW; 4C5BAB1DD346C925 CRC64;

Query Match 85.7%; Score 66; DB 2; Length 1637;
Best Local Similarity 83.3%; Pred. No. 0.72;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRS CG 12
DB 648 WSAWSPCSRS CG 659

RESULT 13

Q7Z292 PRELIMINARY; PRT; 125 AA.
AC Q7Z292
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Adams family protein 2, isoform b.
GN Name-adt-2; ORFNames=PF08C6.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid F08C6.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL EMBL; U29378; AAP40540.1; --
DR WormBase; WBGene0000083; adt-2.
DR WormPep; PF08C6.1b; C333991.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP 1; 2.
DR SMART; SM00209; TSP1; 2.
DR PROSITE; PS00092; TSP1; 2.
SQ SEQUENCE 125 AA; 13940 MW; C572F021D887A468 CRC64;

Query Match 84.4%; Score 65; DB 2; Length 125;
Best Local Similarity 83.3%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRS CG 12
DB 26 WSGWSSCSRS CG 37

RESULT 14

O76510 PRELIMINARY; PRT; 238 AA.
AC O76510
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thrombospondin-related adhesive protein (Fragment).
GN Name=TRAP-C3;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida;
OC Cryptosporidiidae; Cryptosporidium.

Fri Apr 1 15:03:06 2005

Job time : 77.6522 secs

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OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Moredu;
RA Spano F., Putignani L., Crisanti A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF073838; AAC26812.1; -.
DR HSSP; P07996; 1LSL.
DR InterPro; IPR002086; Aldehyd_dehydrog.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP_1; 3.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00092; TSP1; 3.
FT NON_TER 1
FT NON_TER 238
SQ SEQUENCE 238 AA; 26307 MW; 28242D888F62C5A2 CRC64;

Query Match 84.4%; Score 65; DB 2; Length 238;
Best Local Similarity 75.0%; Pred. No. 0.18;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WSGWSCSRSCG 12
Db 47 WSSWSACSKSCG 58

RESULT 15
Q9TTSS PRELIMINARY; PRT; 685 AA.
AC Q9TTSS;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SCO-spondin (Fragment).
GN Name=sco-spondin;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Subcommisural organ;
RA Gobron S., Creveaux I., Monnerie H., Elbitar F.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132106; CABS3759.1; -.
DR HSSP; Q90248; 1HX2.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR003041; PMP_SGI.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP1.
DR InterPro; IPR006552; VMC_out.
DR Pfam; PF01826; TIL; 2.
DR Pfam; PF00090; TSP_1; 6.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1; 6.
DR SMART; SM00215; VMC_out; 1.
DR PROSITE; PS00092; TSP1; 6.
FT NON_TER 1
FT NON_TER 685
SQ SEQUENCE 685 AA; 71389 MW; A003F880E746D5D3 CRC64;

Query Match 84.4%; Score 65; DB 2; Length 685;
Best Local Similarity 83.3%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WSGWSCSRSCG 12
Db 341 WGPWSCSRSCG 352
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Search completed: April 1, 2005, 13:59:23

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:43:07 ; Search time 16.6957 Seconds
(without alignments)
69.156 Million cell updates/sec

Title: US-09-462-909D-8

Perfect score: 77

Sequence: 1 WSGWSCSRSCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	87.0	1444	T18856	angiogenesis inhib
2	65	84.4	957	T15976	hypothetical prote
3	64	83.1	2098	T18397	protein C1RP - mal
4	61	79.2	551	T16557	hypothetical prote
5	61	79.2	860	T16892	hypothetical prote
6	61	79.2	1572	T20027	brain-specific ang
7	60	77.9	1059	T22545	hypothetical prote
8	60	77.9	1170	TSHUP1	thrombospondin 1 p
9	59	76.6	807	A38152	F-spondin - rat
10	58	75.3	654	T29247	hypothetical prote
11	58	75.3	803	A47723	F-spondin precursor
12	58	75.3	1170	A40558	thrombospondin 1 p
13	58	75.3	1172	TSHUP2	thrombospondin 2 p
14	58	75.3	1172	A42587	thrombospondin 2 p
15	58	75.3	1178	A39804	thrombospondin pre
16	57	74.0	651	T19477	hypothetical prote
17	57	74.0	724	A48569	antigen Em100 - Ei
18	56	72.7	788	T25061	hypothetical prote
19	56	72.7	805	T34212	hypothetical prote
20	56	72.7	1184	T09484	cartilage intermed
21	56	72.7	1584	T00026	brain-specific ang
22	55	71.4	919	T32541	unc-5 protein - Ca
23	55	71.4	947	B44294	unc-5 protein, lon
24	55	71.4	984	T00326	hypothetical prote
25	55	71.4	1522	T00028	brain-specific ang
26	55	71.4	2165	T21371	hypothetical prote
27	54	70.1	350	T47158	hypothetical prote
28	54	70.1	610	T16761	hypothetical prote
29	54	70.1	837	T00355	hypothetical prote

Gene ADAMTS-1 prot
semaphorin F prece
coccioidis-relate
immunodominant mic
hypothetical prote
hypothetical prote
procollagen N-endo
TRAP-C2 protein -
hypothetical prote
hypothetical prote
complement C6 prec
hypothetical prote
NOV protein - chic
gene CYR61 protein
hypothetical prote
thrombospondin-rel

ALIGNMENTS

RESULT 1

T18856

angiogenesis inhibitor homolog - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18856; T24653

R:McMurray, A.

submitted to the EMBL Data Library, July 1995

A:Reference number: Z19031

A:Accession: T18856

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1444 <W1L>

A:Cross-references: UNIPROT:Q8MYA8; EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN000028; CESP:CO2B4.1

A:Experimental source: clone C02B4

R:McMurray, A.

submitted to the EMBL Data Library, July 1995

A:Reference number: Z19917

A:Accession: T24653

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1444 <W12>

A:Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN000028; CESP:CO2B4.1

A:Experimental source: clone T07C5

C:Genetics:

A:Gene: CESP:CO2B4.1

A:Map position: X

A:Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566/3

Query Match 87.0%; Score 67; DB 2; Length 1444;

Best Local Similarity 83.3%; Pred. No. 0.12; Indels 0; Gaps 0;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSCSRSCG 12

Db 1071 WSGWSCSRSCG 1082

RESULT 2

T15976

hypothetical protein F08C6.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T15976

R:Bentley, D.

submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid F08C6.

A:Reference number: Z18440

A:Accession: T15976

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-957 <BEN>

A;CROSS-references: UNIPROT:Q19204; EMBL:U29378; NID:g868184; PID:g868185; PIDN:AAA6872
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CRSP:P08C6.1
A;Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3; 461/2; 498/3; 532/3; 627/2; 714/1; 7

Query Match 84.4%; Score 65; DB 2; Length 957;
Best Local Similarity 83.3%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRS CG 12
DB 858 WSGWSQC SVSCG 869

RESULT 3
Tl8397 protein CTRP - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: Tl8397
R;Tröttelein, F.; Trögler, T.; Cowman, A.F.
Mol. Biochem. Parasitol. 74, 129-142, 1995
A;Title: Molecular cloning of a gene from Plasmodium falciparum that codes for a protein
A;Reference number: Z18926; MUID:96360471; PMID:8719155
A;Accession: Tl8397
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2098 <TRO>
A;CROSS-references: UNIPROT:Q25757; EMBL:U34363; NID:g1098897; PID:g1098898; PIDN:AAC469

Query Match 83.1%; Score 64; DB 2; Length 2098;
Best Local Similarity 75.0%; Pred. No. 0.42;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRS CG 12
DB 1644 WSDWSSCSKTCG 1655

RESULT 4
Tl6557 hypothetical protein K04E7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: Tl6557
R;Nhan, M.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid K04E7.
A;Reference number: Z18535
A;Accession: Tl6557
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-551 <NHA>
A;CROSS-references: UNIPROT:P55114; EMBL:U39666; NID:g1049408; PID:g1049411; PIDN:AAA804
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CRSP:K04E7.3
A;Introns: 43/3; 81/3; 112/3; 153/1; 191/2; 213/3; 241/2; 281/3; 324/1; 364/1; 393/3; 4
C;Superfamily: metalloproteinase hch-1; astacin homology

Query Match 79.2%; Score 61; DB 2; Length 551;
Best Local Similarity 66.7%; Pred. No. 0.39;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRS CG 12
DB 491 WSGWTRCSENCG 502

RESULT 5
Tl6892 hypothetical protein Tl9D2.1 - Caenorhabditis elegans

```

C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16892
R;Bentley, D.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid T19D2.
A;Reference number: Z18599
A;Accession: T16892
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-860 <BN>
A;Cross-references: UNIPROT:Q22580; EMBL:U42846; NID:g1125809; PID:g1125810; PIDN:AAA8360
C;Genetics:
A;Gene: CESP:T19D2.1
A;Introns: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 582/3
Query Match 79.2%; Score 61; DB 2; Length 860;
Best Local Similarity 75.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSQ 12
DB 831 WSSWSSCTKCG 842

RESULT 6
T00027
brain-specific angiogenesis inhibitor 2 - human
N;Alternate names: BA12 protein
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00027
R;Shiratachi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.
Cytoenet. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BA12 and BA13, novel genes homologous to brain-
A;Reference number: Z14066; MUID:98194217; PMID:9533023
A;Accession: T00027
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1572 <SH>
A;Cross-references: UNIPROT:O60241; EMBL:AB005298; NID:g3021698; PIDN:BA25362.1; PID:g3021698
A;Experimental source: brain
C;Genetics:
A;Gene: GDB:BA12
A;Cross-references: GDB:9838089; OMIM:602683
A;Map position: lp35-1p35

Query Match 79.2%; Score 61; DB 2; Length 1572;
Best Local Similarity 75.0%; Pred. No. 0.85;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSQ 12
DB 358 WGSWSLCSRSQ 369

RESULT 7
T22545
hypothetical protein F53B6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22545
R;White, S.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19578
A;Accession: T22545
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1059 <WL>
A;Cross-references: UNIPROT:P90884; EMBL:Z81086; PIDN:CAB03121.1; GSPDB:GN00019; CESP:F53B6
A;Experimental source: clone F53B6
C;Genetics:
A;Gene: CESP:F53B6.2

```

A;Map position: 1
A;Introns: 38/3; 92/3; 131/3; 169/1; 236/2; 282/3; 349/2; 376/2; 420/1; 576/3; 759/3; 84

Query Match 77.9%; Score 60; DB 2; Length 1059;
Best Local Similarity 66.7%; Pred. No. 0.87;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||| :|||
Db 29 WSPWSSCTTCG 40

RESULT 8
TSHUP1
C;Species: Homo sapiens - human
C;Date: 23-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A26155; A34274; A30140; A25812; A05172; A42927
R;Lawler, J.; Hynes, R.O.
J. Cell Biol. 103, 1635-1648, 1986
A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple
A;Reference number: A26155; MUID:87057617; PMID:2430973
A;Accession: A26155
A;Molecule type: mRNA
A;Residues: 1-1170 <LAW>
A;Cross-references: UNIPROT:P07996; GB:X04665; NID:G37137; PIDN:CRA28370.1; PID:G37138
A;Note: parts of this sequence, including the amino end of the mature protein, were deter
R;Laherty, C.D.; Giernan, T.M.; Dixit, V.M.
J. Biol. Chem. 264, 11222-11227, 1989
A;Title: Characterization of the promoter region of the human thrombospondin gene. DNA
A;Reference number: A34274; MUID:89291870; PMID:2544587
A;Accession: A34274
A;Molecule type: DNA
A;Residues: 1-166 <LAH>
A;Cross-references: GB:J04835
R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein,
J. Cell Biol. 108, 729-736, 1989
A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in th
A;Reference number: A30140; MUID:89139590; PMID:2918029
A;Accession: A30140
A;Molecule type: mRNA
A;Residues: 1-83, 'A', '85-522, 'A', '524-1170 <HEN>
A;Cross-references: EMBL:X14787; NID:G37464; PIDN:CAA32889.1; PID:G37465
A;Note: parts of this sequence, including the amino end of the mature protein, were deter
R;Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A;Title: Partial amino acid sequence of human thrombospondin as determined by analysis o
A;Reference number: A25812; MUID:87157592; PMID:3030396
A;Accession: A25812
A;Molecule type: mRNA
A;Residues: 1-83, 'A', '85-397 <KOB>
A;Cross-references: GB:M25631; NID:G538353; PIDN:AAA36741.1; PID:G538354
R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
A;Reference number: A05172; MUID:86287276; PMID:3461443
A;Accession: A05172
A;Molecule type: mRNA
A;Residues: 1-83, 'A', '85-374, 'RC' <DIX>
A;Cross-references: GB:M14326; NID:G340005; PIDN:AAA61237.1; PID:G553801
A;Note: parts of this sequence, including the amino end of the mature protein, were deter
R;Sun, X.; Skortenggaard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A;Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A;Reference number: A42927; MUID:92348511; PMID:1379247
A;Accession: A42927
A;Molecule type: protein
A;Residues: 987-1003 <SUN>
A;Note: Cys-992 is shown to have a free sulfhydryl
C;Genetics:
A;Gene: GDB:THBS1; TSP1; TSP
A;Cross-references: GDB:120438; OMIM:180606
A;Map position: 15q15-15q15
A;Introns: 23/1

A;Note: the list of introns may be incomplete
C;Complex: homotrimer, disulfide linked
C;Function:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F;551-586/Domain: EGF homology <EGF1>
F;650-689/Domain: EGF homology <EGF2>
F;926-928/Region: cell attachment (R-G-D) motif
F;171-232/Disulfide bonds: #status predicted
F;248,360,708,1067/Binding site: carboxydrate (Asn) (covalent) #status predicted
F;270,274/Disulfide bonds: interchain #status predicted
F;610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;1051/Binding site: carboxydrate (Asn) (covalent) #status absent

Query Match 77.9%; Score 60; DB 1; Length 1170;
Best Local Similarity 75.0%; Pred. No. 0.93;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||| :|||
Db 385 WSEWTSCTSCG 396

RESULT 9
A38152
F-spondin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A38152
R;Klar, A.; Baldassare, M.; Jessell, T.M.
Cell 69, 95-110, 1992
A;Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secreted
A;Reference number: A38152; MUID:92208952; PMID:1555244
A;Accession: A38152
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-807 <KLA>
A;Cross-references: UNIPROT:P35446; GB:M88469; NID:G204176; PIDN:AAA41174.1; PID:G204177
A;Note: sequence extracted from NCBI backbone (NCBIN:90877, NCBI:90878)
C;Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;441-495/Domain: thrombospondin type 1 repeat homology <THR2>
F;500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F;557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F;613-666/Domain: thrombospondin type 1 repeat homology <THR1>
F;667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F;753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 76.6%; Score 59; DB 2; Length 807;
Best Local Similarity 66.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||| :|||
Db 674 WSGWSECNKSCG 685

RESULT 10
T29247
hypothetical protein F09F9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29247
R;Minx, P.; Hawkins, J.
Submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F09F9.

Fri Apr 1 15:03:06 2005

us-09-462-909d-8.rpr

```
J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: B42587
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1152; P' 1154-1170 <LAH>
A;Cross-references: GB:M87776
A;Note: sequence extracted from NCBI backbone (NCBIP:81501)
R;Chen, H.; Aschlimann, D.; Nowlen, J.; Mosner, D.F.
FBS Lett. 387, 36-41, 1996
A;Title: Expression and initial characterization of recombinant mouse thrombospondin 1 ar
A;Reference number: S68787; MUID:96234006; PMID:8654563
A;Accession: S68787
A;Molecule type: protein
A;Residues: 19-26; X' 28-37 <CHE>
C;Complex: homotrimer, disulfide linked
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
C;Keywords: calcium binding; glycoprotein; homotrimer
F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F;551-586/Domain: EGF homology <EGF>
F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.3%; Score 58; DB 2; Length 1170;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||| ||| ||| |||
Db 441 WSPWSSCSVTCG 452

RESULT 13
TSHUP2
thrombospondin 2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A47379; A42173
R;LaBell, T.L.; Byers, P.H.
Genomics 17, 225-229, 1993
A;Title: Sequence and characterization of the complete human thrombospondin 2 cDNA: poter
A;Reference number: A47379; MUID:94010892; PMID:8406456
A;Accession: A47379
A;Molecule type: mRNA
A;Residues: 1-1172 <LAB>
A;Cross-references: UNIPROT:P35442; GB:112350; NID:G307505; PIDN:AAA03703.1; PID:G307506
R;LaBell, T.L.; Milewicz, D.J.; Distche, C.M.; Byers, P.H.
Genomics 12, 421-429, 1992
A;Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression of
A;Reference number: A42173; MUID:92217961; PMID:1559694
A;Accession: A42173
A;Molecule type: mRNA
A;Residues: 560-1172 <LA2>
A;Cross-references: GB:M81339
A;Experimental source: fibroblast
A;Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
C;Genetics:
A;Gene: GDB:THRS2; TSP2
A;Cross-references: GDB:128789; OMIM:188061
A;Map position: 6q27-6q27
C;Complex: homotrimer, disulfide linked
C;Function:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1172/Product: thrombospondin 2 #status predicted <MAT>
F;319-377/Domain: von Willebrand factor type C repeat homology <VWC>
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A;Reference number: Z20594
A;Accession: T29247
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-654 <MIN>
A;Cross-references: UNIPROT:Q19284; EMBL:U40958; PIDN:AAA81764.1; CESP:F09F9.4
A;Gene: CESP:F09F9.4
A;Introns: 89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1; 523/1; 558/2; 596/2

Query Match 75.3%; Score 58; DB 2; Length 654;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||| ||| ||| |||
Db 322 WSEWSSCSVTCG 333

RESULT 11
F-spondin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A47723
R;Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A;Title: Ectopic neural expression of a floor plate marker in frog embryos injected with
A;Reference number: A47723; MUID:93376785; PMID:8367492
A;Accession: A47723
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-803 <RUL>
A;Cross-references: UNIPROT:P35447; GB:L09123; NID:G409244; PIDN:AAA19105.1; PID:G409245
C;Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;435-489/Domain: thrombospondin type 1 repeat homology <THR2>
F;607-662/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 75.3%; Score 58; DB 2; Length 803;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
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Db 670 WSWWSSCSVTCG 681

RESULT 12
thrombospondin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42587; S68787
R;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
Genomics 11, 587-600, 1991
A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUID:92128941; PMID:1774063
A;Accession: A40558
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1170 <LAW>
A;Cross-references: UNIPROT:P35441; GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M6245
; GB:M62464; GB:M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:G5118
R;Bornstein, P.; Alfli, D.; Devarayala, S.; Franson, P.; Li, P.
J. Biol. Chem. 265, 16691-16698, 1990
A;Title: Characterization of the mouse thrombospondin gene and evaluation of the role of
A;Reference number: A37905; MUID:90375546; PMID:2398070
A;Accession: A37905
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-490 <BOR>
A;Cross-references: GB:J05605; GB:J05606; NID:G201991; PIDN:AAA40431.1; PID:G554390
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
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F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>
 F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
 F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
 F;553-588/Domain: EGF homology <EGF1>
 F;652-691/Domain: EGF homology <EGF>
 F;928-930/Region: cell attachment (R-G-D) motif
 F;151-316,330,457,584,710,1069/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;167-226/Disulfide bonds: #status predicted
 F;266-270/Disulfide bonds: interchain #status predicted
 F;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 75.3%; Score 58; DB 1; Length 1172;
 Best Local Similarity 75.0%; Pred. No. 1.7;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
 DB 443 WSPWSSCSVTGC 454

RESULT 14

A42587
 thrombospondin 2 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A42587; A39851
 R:LaHerty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
 J. Biol. Chem. 267, 3274-3281, 1992
 A:Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
 A:Reference number: A42587; MUID:92147683; PMID:1371115
 A:Accession: A42587
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-1172 <LA>
 A:Cross-references: UNIPROT:Q03350; GB:L07803; GB:M87275; NID:G340421; PIDN:AAA53064.1;
 R:Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.
 J. Biol. Chem. 266, 12821-12824, 1991
 A:Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.
 A:Reference number: A39851; MUID:91302287; PMID:1712771

A:Accession: A39851
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-873 <BOR>
 A:Cross-references: GB:M64866; NID:G201994; PIDN:AAA40432.1; PID:G201995
 C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v
 C:Keywords: calcium binding; glycoprotein
 F;319-377/Domain: von Willebrand factor type C repeat homology <VMC>
 F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>
 F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
 F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
 F;553-588/Domain: EGF homology <EGF1>
 F;652-691/Domain: EGF homology <EGF>

Query Match 75.3%; Score 58; DB 2; Length 1172;
 Best Local Similarity 75.0%; Pred. No. 1.7;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
 DB 443 WSPWSSCSVTGC 454

RESULT 15

A39804
 thrombospondin precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A39804
 R:Lawler, J.; Duquette, M.; Ferro, P.
 J. Biol. Chem. 266, 8039-8043, 1991
 A:Title: Cloning and sequencing of chicken thrombospondin.
 A:Reference number: A39804; MUID:91217026; PMID:2022631

A:Accession: A39804
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1178 <LA>
 A:Cross-references: UNIPROT:P35440; GB:M60853; NID:G212763; PIDN:AAA51437.1; PID:G212764
 C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v
 F;325-383/Domain: von Willebrand factor type C repeat homology <VMC>
 F;386-437/Domain: thrombospondin type 1 repeat homology <THR1>
 F;442-498/Domain: thrombospondin type 1 repeat homology <THR2>
 F;499-555/Domain: thrombospondin type 1 repeat homology <THR3>
 F;658-697/Domain: EGF homology <EGF>

Query Match 75.3%; Score 58; DB 1; Length 1178;
 Best Local Similarity 75.0%; Pred. No. 1.8;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
 DB 449 WSPWSSCSVTGC 460

Search completed: April 1, 2005, 14:00:30
 Job time : 16.6957 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:59:39 ; Search time 61.8261 Seconds
(without alignments)
64.360 Million cell updates/sec

Title: US-09-462-909D-8

Perfect score: 77

Sequence: 1 WSGWSSCSRSCG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 segs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications-AA.*

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	88.3	4123	14 US-10-213-509-5	Sequence 5, Appli
2	68	88.3	4219	15 US-10-085-198-2	Sequence 2, Appli
3	65	84.4	997	9 US-09-918-171A-7	Sequence 7, Appli
4	65	84.4	997	10 US-09-981-151A-32	Sequence 32, Appl
5	65	84.4	997	16 US-10-408-765A-1094	Sequence 1094, Ap
6	65	84.4	1255	15 US-10-312-352-23	Sequence 23, Appl
7	65	84.4	1686	15 US-10-386-414-2	Sequence 2, Appli
8	65	84.4	1690	9 US-09-788-043C-5	Sequence 5, Appli
9	64	83.1	353	15 US-10-161-493-132	Sequence 132, App
10	63	81.8	415	10 US-09-800-198-89	Sequence 89, Appl
11	63	81.8	571	15 US-10-262-839-180	Sequence 180, App
12	63	81.8	577	15 US-10-262-839-196	Sequence 196, App
13	63	81.8	791	10 US-09-981-151A-4	Sequence 4, Appli

14	63	81.8	856	10 US-09-981-151A-6	Sequence 6, Appli
15	63	81.8	952	10 US-09-981-151A-8	Sequence 8, Appli
16	63	81.8	986	10 US-09-981-151A-2	Sequence 2, Appli
17	63	81.8	1224	13 US-10-217-774-4	Sequence 4, Appli
18	63	81.8	1224	14 US-10-296-616-2	Sequence 2, Appli
19	63	81.8	1224	15 US-10-275-107-51	Sequence 51, Appl
20	63	81.8	1224	17 US-10-804-457-4	Sequence 4, Appli
21	63	81.8	1236	15 US-10-399-645-4	Sequence 4, Appli
22	63	81.8	1365	15 US-10-120-801-48	Sequence 48, Appl
23	63	81.8	1490	15 US-10-262-839-184	Sequence 184, App
24	63	81.8	1545	15 US-10-262-839-182	Sequence 182, App
25	63	81.8	1549	15 US-10-262-839-186	Sequence 186, App
26	63	81.8	1588	13 US-10-000-512-2	Sequence 2, Appli
27	63	81.8	1588	15 US-10-074-566-2	Sequence 41, Appli
28	63	81.8	1588	15 US-10-262-839-176	Sequence 176, App
29	63	81.8	1588	15 US-10-262-839-188	Sequence 188, App
30	63	81.8	1588	15 US-10-262-839-194	Sequence 194, App
31	63	81.8	1588	15 US-10-262-839-200	Sequence 200, App
32	63	81.8	1624	17 US-10-363-374-6	Sequence 6, Appli
33	62	80.5	349	15 US-10-161-493-126	Sequence 126, App
34	62	80.5	353	15 US-10-161-493-138	Sequence 138, App
35	62	80.5	353	15 US-10-161-493-130	Sequence 130, App
36	62	80.5	353	15 US-10-161-493-134	Sequence 134, App
37	62	80.5	661	15 US-10-354-983-8	Sequence 8, Appli
38	62	80.5	862	14 US-10-226-560-2	Sequence 2, Appli
39	62	80.5	914	15 US-10-188-186-132	Sequence 132, App
40	62	80.5	919	15 US-10-188-186-130	Sequence 130, App
41	62	80.5	934	15 US-10-275-107-53	Sequence 53, Appl
42	62	80.5	1071	15 US-10-354-983-4	Sequence 4, Appli
43	62	80.5	1081	15 US-10-120-801-46	Sequence 46, Appl
44	62	80.5	1081	15 US-10-391-364-87	Sequence 87, Appl
45	62	80.5	1081	16	

ALIGNMENTS

RESULT 1
US-10-213-509-5
; Sequence 5, Application US/10213509
; Publication No. US20030054485A1
; GENERAL INFORMATION:
; APPLICANT: Weiss, Joseph
; APPLICANT: Scott, Matthew
; TITLE OF INVENTION: JELLY BELLY GENES AND THEIR USES
; FILE REFERENCE: STAN-232
; CURRENT APPLICATION NUMBER: US/10/213,509
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/311,720
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; TYPE: PRT
; LENGTH: 4123
; ORGANISM: H. sapiens
; US-10-213-509-5

Query Match 88.3%; Score 68; DB 14; Length 4123;
Best Local Similarity 91.7%; Pred. No. 4.8;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
Db 2518 WSGWSSCSRSCG 2529

RESULT 2
US-10-085-198-2
; Sequence 2, Application US/10085198
; Publication No. US2004000907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.

RESULT 4
US-09-981-151A-32
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-2

Query Match 88.3%; Score 68; DB 15; Length 4219;
Best Local Similarity 91.7%; Pred. No. 4.9;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
||| |||||
Db 2614 WSVWSSCSRSCG 2625

RESULT 3
US-09-918-171A-7
; Sequence 7, Application US/09918171A
; Patent No. US2002011089A1
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurekainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/04193
; CURRENT APPLICATION NUMBER: US/09/918,171A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/369,364
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-7
US-09-918-171A-7

Query Match 84.4%; Score 65; DB 9; Length 997;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
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Db 544 WSAWSICSRSCG 555

US-09-981-151A-32
; Sequence 32, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glenna
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-151A-32

Query Match 84.4%; Score 65; DB 10; Length 997;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
||| |||||
Db 544 WSAWSICSRSCG 555

RESULT 5
US-10-408-765A-1094
; Sequence 1094, Application US/10408765A
; Publication No. US20040101874A1

GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1094
LENGTH: 997
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-1094

Query Match 84.4%; Score 65; DB 16; Length 997;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
DB 544 WSAWSICSRSCG 555

RESULT 6

US-10-312-352-23
Sequence 23, Application US/10312352
Publication No. US20040053824A1
GENERAL INFORMATION:
APPLICANT: INCITE GENOMICS, INC.; TANG, Y. Tom
APPLICANT: YUE, Henry; AZIMZAI, Yalda
APPLICANT: HE, Ann; BAPRA, Sajeev
APPLICANT: LO, Terence P.; NGUYEN, Dannel B.
APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.
APPLICANT: LAL, Preeti G.; KEARNEY, Liam
APPLICANT: BURFORD, Neil; YAO, Monique G.
APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.
APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.
APPLICANT: BAUGHN, Mariah R.; HAFALIA, April, J.A.
APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
APPLICANT: LU, Yan; BOROWSKI, Mark L.
APPLICANT: LU, Dyung Aina M.; RAMKUMAR, Jayalaxmi
APPLICANT: YANG, Junming; GURURAJAN, Rajagopal
APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.
APPLICANT: XU, Yuming; KALLICK, Deborah A.
APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha
APPLICANT: DELEGANE, Angelo M.; LEE, Sally
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
FILE REFERENCE: PF-0794 USN
CURRENT APPLICATION NUMBER: US/10/312,352
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: PCT/US01/21067
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,454
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/219,462
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 60/240,111
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/240,106
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/244,021
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/248,887
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/249,570

PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PERL Program
SEQ ID NO 23
LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040053824A1 55022490CD1
US-10-312-352-23

Query Match 84.4%; Score 65; DB 15; Length 1255;
Best Local Similarity 83.3%; Pred. No. 4.5;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
DB 113 WSAWSICSRSCG 124

RESULT 7

US-10-386-414-2
Sequence 2, Application US/10386414
Publication No. US20040006016A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Robison, Keith E.
APPLICANT: White, David
APPLICANT: Williamson, Mark W.
APPLICANT: Cook, William James
APPLICANT: Meyers, Rachel E.
APPLICANT: Macbeth, Kyle J.
APPLICANT: Carroll, Joseph M.
APPLICANT: Chun, Miyoung
TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
FILE REFERENCE: MPI03-0210WNIM
CURRENT APPLICATION NUMBER: US/10/386,414
CURRENT FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: 09/426,282
PRIOR FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 09/668,266
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/330,970
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 09/724,599
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/860,193
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 10/283,023
PRIOR FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 60/335,044
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 10/010,943
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/254,037
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/833,082
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1686
TYPE: PRT
ORGANISM: Homo Sapien
US-10-386-414-2

Query Match 84.4%; Score 65; DB 15; Length 1686;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12

us-09-462-909d-8.rapb

Fri Apr 1 15:03:05 2005

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; FILE REFERENCE: 21402-377A
; CURRENT APPLICATION NUMBER: US/10/161,493
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/337,524
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,575
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/359,151
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,573
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/341,143
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 299
; SEQ ID NO 132
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-161-493-132

Query Match      83.1%; Score 64; DB 15; Length 353;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 WSGWSSCSRSCG 12
DB      303 WSNWSECSRTCG 314

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RESULT 10
US-09-800-198-89
; Sequence 89, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Cornie AM
; APPLICANT: Bernades, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Hermann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishna
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Halocynthia roretzi
; US-09-800-198-89

Query Match      81.8%; Score 63; DB 10; Length 415;
Best Local Similarity 75.0%; Pred. No. 3.3;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 WSGWSSCSRSCG 12
DB      303 WSNWSECSRTCG 314

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; FILE REFERENCE: 21402-377A
; CURRENT APPLICATION NUMBER: US/10/161,493
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/337,524
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,575
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/359,151
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,573
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/341,143
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 299
; SEQ ID NO 132
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-161-493-132

Query Match      83.1%; Score 64; DB 15; Length 353;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 WSGWSSCSRSCG 12
DB      303 WSNWSECSRTCG 314

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RESULT 10
US-09-800-198-89
; Sequence 89, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Cornie AM
; APPLICANT: Bernades, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Hermann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishna
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Halocynthia roretzi
; US-09-800-198-89

Query Match      81.8%; Score 63; DB 10; Length 415;
Best Local Similarity 75.0%; Pred. No. 3.3;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 WSGWSSCSRSCG 12
DB      303 WSNWSECSRTCG 314

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Db 124 WSNWSRCSKSCG 135

RESULT 12

US-10-262-839-196
; Sequence 196, Application US/10262839
; Publication No. US20040038877A1
; GENERAL INFORMATION:

; GENERAL INFORMATION:
 ; APPLICANT: Alsbrook, John,
 ; APPLICANT: Anderson, David W.,
 ; APPLICANT: Boldog, Ferenc,
 ; APPLICANT: Burgess, Catherine,
 ; APPLICANT: Catterton, Elina,
 ; APPLICANT: Edinger, Shlomit,
 ; APPLICANT: Ellerman, Karen,
 ; APPLICANT: Gerlach, Valerie,
 ; APPLICANT: Gorman, Linda,
 ; APPLICANT: Guo, Xiaojia,
 ; APPLICANT: Ji, Weizhen,
 ; APPLICANT: Kekuda, Ramesh,
 ; APPLICANT: Leach, Martin,
 ; APPLICANT: Li, Li,
 ; APPLICANT: Miller, Charles,
 ; APPLICANT: Patturajan, Meera,
 ; APPLICANT: Reiger, Daniel,
 ; APPLICANT: Rothenberg, Mark,
 ; APPLICANT: Shimkets, Richard,
 ; APPLICANT: Smithson, Glenda,
 ; APPLICANT: Spytek, Kimberly,
 ; APPLICANT: Taupier, Raymond, jr.,
 ; APPLICANT: Vernet, Corine,
 ; APPLICANT: Voss, Edward,
 ; APPLICANT: Zerhusen, Brian,
 ; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
 ; FILE REFERENCE: 21402-463A

1125 REFERENCE: Z1102 1024
: CURRENT APPLICATION NUMBER: US/10/262.839

1	CURRENT FILING DATE:	2002-10-01	60/326,483
2	PRIOR APPLICATION NUMBER:	60/326,483	
3	PRIOR FILING DATE:	2001-10-02	60/327,917
4	PRIOR APPLICATION NUMBER:	60/327,917	
5	PRIOR FILING DATE:	2001-10-09	60/328,029
6	PRIOR APPLICATION NUMBER:	60/328,029	
7	PRIOR FILING DATE:	2001-10-09	60/328,056
8	PRIOR APPLICATION NUMBER:	60/328,056	
9	PRIOR FILING DATE:	2001-10-09	60/381,101
10	PRIOR APPLICATION NUMBER:	60/381,101	
11	PRIOR FILING DATE:	2002-05-16	60/371,972
12	PRIOR APPLICATION NUMBER:	60/371,972	
13	PRIOR FILING DATE:	2002-04-12	60/327,342
14	PRIOR APPLICATION NUMBER:	60/327,342	
15	PRIOR FILING DATE:	2001-10-05	60/328,044
16	PRIOR APPLICATION NUMBER:	60/328,044	
17	PRIOR FILING DATE:	2001-10-09	60/328,849
18	PRIOR APPLICATION NUMBER:	60/328,849	
19	PRIOR FILING DATE:	2001-10-12	60/374,738
20	PRIOR APPLICATION NUMBER:	60/374,738	

REMAINING PRIOR APPLICATION DATA REMOVED - SEE FILE WRAPPER OR PALM

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; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: CuraSeqList version 0.1

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: SEO ID NO 196

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; LENGTH: 577
; TYPE: PRT

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ORGANISM: *Homo sapiens*

US-10-262-839-196

Query Match 81.8%; Score 63; DB 15; Length 577;
Best Local Similarity 75.0%; Pred. No. 4.3;
Matches 9: Conservative 1: Mismatches 2: Indels

Ov 1 WSGWSSCSPSCG 12

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Fri Apr 1 15:03:05 2005

Db 125 WSNWRSKSCG 136

RESULT 13

US-09-981-151A-4
; Sequence 4, Application US/09981151A
; Publication No. US20030212256A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-168

; CURRENT APPLICATION NUMBER: US/09/981,151A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 60/241,040

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/241,058

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/241,063

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/241,243

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/242,152

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/242,482

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/242,611

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/242,612

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/242,880

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: 60/242,881

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 4

; LENGTH: 791

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-981-151A-4

Query Match 81.8%; Score 63; DB 10; Length 791;

Best Local Similarity 75.0%; Pred. No. 5.5;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12

Db 477 WSSWSPCSRTCG 488

RESULT 14

US-09-981-151A-6

; Sequence 6, Application US/09981151A

; Publication No. US20030212256A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-168

; CURRENT APPLICATION NUMBER: US/09/981,151A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 60/241,040

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/241,058

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/241,063

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/241,243

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/242,152

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/242,482

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/242,611

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/242,612

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/242,880

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: 60/242,881

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 6

; LENGTH: 856

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-981-151A-6

Query Match 81.8%; Score 63; DB 10; Length 856;

Best Local Similarity 75.0%; Pred. No. 5.9;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12

Db 543 WSSWSPCSRTCG 554

RESULT 15

US-09-981-151A-8

; Sequence 8, Application US/09981151A

; Publication No. US20030212256A1

; GENERAL INFORMATION:

Fri Apr 1 15:03:05 2005

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; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 952
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-981-151A-8

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Query Match      81.8%; Score 63; DB 10; Length 952;
Best Local Similarity 75.0%; Pred. No. 6.4;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 WSGWSSCSRSCG 12
Db      629 WSSWSPCSRTCG 640

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Search completed: April 1, 2005, 14:22:17
Job time : 61.8261 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:44:22 ; Search time 21.1304 Seconds
(without alignments)
42.393 Million cell updates/sec

Title: US-09-462-909D-8
Perfect score: 77
Sequence: 1 WSGWSCSRSCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	63	81.8	1224	4	US-09-930-872-4
3	63	81.8	1224	4	US-10-217-774-4
4	60	77.9	23	1	US-07-646-531D-5
5	60	77.9	23	2	US-08-488-273-5
6	60	77.9	23	3	US-09-197-770B-11
7	60	77.9	23	6	5426100-5
8	60	77.9	23	6	5426100-5
9	60	77.9	218	3	US-08-985-526-1
10	60	77.9	239	5	PCT-US93-01652-1
11	60	77.9	441	3	US-08-985-526-3
12	60	77.9	1059	4	US-09-800-729-217
13	60	77.9	1170	1	US-08-313-288B-20
14	60	77.9	1170	4	US-09-657-472-2
15	59	76.6	52	2	US-08-799-173A-12
16	59	76.6	52	4	US-09-170-042A-12
17	59	76.6	56	1	US-07-862-021B-19
18	59	76.6	56	5	PCT-US93-03164-19
19	59	76.6	446	4	US-09-784-358-4
20	59	76.6	518	3	US-09-369-364A-22
21	59	76.6	724	4	US-09-784-358-8
22	59	76.6	787	4	US-09-825-294-207
23	59	76.6	787	4	US-09-970-966-207
24	59	76.6	807	1	US-07-862-021B-10
25	59	76.6	807	1	US-08-313-288B-10
26	59	76.6	807	4	US-09-132-769-1
27	59	76.6	807	4	US-09-132-769-3

28	59	76.6	807	4	US-09-132-769-5
29	59	76.6	807	4	US-09-640-173-186
30	59	76.6	807	4	US-09-713-550-186
31	59	76.6	807	4	US-09-825-294-186
32	59	76.6	807	4	US-09-970-966-186
33	59	76.6	807	5	PCT-US93-03164-10
34	59	76.6	845	4	US-09-784-358-12
35	59	76.6	930	4	US-09-122-126B-15
36	59	76.6	930	4	US-09-634-286A-15
37	59	76.6	930	4	US-10-247-685-15
38	59	76.6	1691	4	US-09-784-358-2
39	58	75.3	23	1	US-07-646-531D-6
40	58	75.3	23	2	US-08-488-273-6
41	58	75.3	23	3	US-09-197-770B-12
42	58	75.3	23	6	5426100-6
43	58	75.3	23	6	5426100-6
44	58	75.3	50	4	US-09-800-729-161
45	58	75.3	60	1	US-07-646-531D-12

ALIGNMENTS

RESULT 1
US-09-369-364A-7
; Sequence 7, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-7
US-09-369-364A-7

Query Match 84.4%; Score 65; DB 3; Length 997;
Best Local Similarity 83.3%; Pred. No. 2, 4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSCSRSCG 12
Db 544 WSAWSICSRSCG 555

RESULT 2
US-09-930-872-4
; Sequence 4, Application US/09930872
; Patent No. 6448388
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6448388el Human Proteases and Polynucleotides Encoding the San
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/09/930,872
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1224
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-930-872-4

Query Match 81.8%; Score 63; DB 4; Length 1224;
Best Local Similarity 75.0%; Pred. No. 4.9;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
DB 592 WSSWSPCSRSCG 603

RESULT 3
US-10-217-774-4
; Sequence 4, Application US/10217774
; Patent No. 6734007
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT FILING DATE: 2002-08-12
; PRIOR FILING DATE: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1224
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-217-774-4

Query Match 81.8%; Score 63; DB 4; Length 1224;
Best Local Similarity 75.0%; Pred. No. 4.9;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
DB 592 WSSWSPCSRSCG 603

RESULT 4
US-07-646-531D-5
; Sequence 5, Application US/07646531D
; Patent No. 5200397
; GENERAL INFORMATION:
; APPLICANT: Deutch, Alan Howard
; APPLICANT: Tuszyński, George Paul
; TITLE OF INVENTION: Peptide fragments and analogs of
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. R. Grace & Co.-Conn.
; STREET: 7379 Route 32
; CITY: Columbia
; STATE: Maryland
; COUNTRY: USA
; ZIP: 21044
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/646,531D
; FILING DATE: 19910131
; ATTORNEY/AGENT INFORMATION:
; NAME: Appleby, Vanessa L.
; REGISTRATION NUMBER: 33223
; REFERENCE/DOCKET NUMBER: 01-7896
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 531-4515

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-646-531D-5

Query Match 77.9%; Score 60; DB 1; Length 23;
Best Local Similarity 75.0%; Pred. No. 0.39;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
DB 4 WSEWTSCTSCG 15

RESULT 5
US-08-488-273-5
; Sequence 5, Application US/08488273
; Patent No. 5840692
; GENERAL INFORMATION:
; APPLICANT: Deutch, Alan H.
; APPLICANT: Tuszyński, George P.
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; TITLE OF INVENTION: THROMBOSPONDIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,273
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/359,263
; FILING DATE: 19-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/896,527
; FILING DATE: 09-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/483,527
; FILING DATE: 22-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-2U4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 567-2020
; TELEFAX: (215) 567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-273-5

Query Match 77.9%; Score 60; DB 2; Length 23;

Best Local Similarity 75.0%; Pred. No. 0.39;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
|||:|||||
Db 4 WSEWTSCTSCG 15

RESULT 6

US-09-197-770B-11
; Sequence 11, Application US/09197770B
; Patent No. 6339062
; GENERAL INFORMATION:
; APPLICANT: Tuszyński, George
; APPLICANT: Williams, Taffy
; APPLICANT: Actor, Paul
; TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT
; TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY
; FILE REFERENCE: 07206-0021
; CURRENT APPLICATION NUMBER: US/09/197,770B
; CURRENT FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: fragment/ analog of thrombospondin
US-09-197-770B-11

Query Match 77.9%; Score 60; DB 3; Length 23;
Best Local Similarity 75.0%; Pred. No. 0.39;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
|||:|||||
Db 4 WSEWTSCTSCG 15

RESULT 7

5426100-5
; Patent No. 5426100
; APPLICANT: DEUTCH, ALAN H.; TUSZYNSKI, GEORGE
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; THROMBOSPONDIN

; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 483,527
; FILING DATE: 22-FEB-1990
; SEQ ID NO:5:
; LENGTH: 23
5426100-5

Query Match 77.9%; Score 60; DB 6; Length 23;
Best Local Similarity 75.0%; Pred. No. 0.39;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
|||:|||||
Db 4 WSEWTSCTSCG 15

RESULT 8

5426100-5
; Patent No. 5426100
; APPLICANT: DEUTCH, ALAN H.; TUSZYNSKI, GEORGE

; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; THROMBOSPONDIN

; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 483,527
; FILING DATE: 22-FEB-1990
; SEQ ID NO:5:
; LENGTH: 23
5426100-5

Query Match 77.9%; Score 60; DB 6; Length 23;
Best Local Similarity 75.0%; Pred. No. 0.39;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
|||:|||||
Db 4 WSEWTSCTSCG 15

RESULT 9

US-08-985-526-1
; Sequence 1, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-1

Query Match 77.9%; Score 60; DB 3; Length 218;
Best Local Similarity 75.0%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
|||:|||||
Db 85 WSEWTSCTSCG 96

Query Match	77.9%;	Score 60;	DB 3;	Length 441;
Best Local Similarity	75.0%;	Pred. No. 4.7;		
Best Overall Similarity	80.0%;	Mismatches 1;	Indels 2;	Gaps 0;
Conservative				

Qy 1 WSGWSSCSRSCG 12
85 WSEWTSCTSCG 96

```

RESULT 12
US-09-800-729-217
; Sequence 217, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
; LENGTH: 1059
; TYPE: prt
; ORGANISM: Homo sapiens
; rs_09-800-729-217

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Query Match	77.9%;	Score 60;	DB 4;	Length 1059;
Best local Similarity	66.7%;	Pred. No. 9.9;		
Matches	8;	Conservative	3;	Mismatches 1; Indels 0; Gaps 0;
QY	1	WSGWSSCSRS	CG	12
				::
	29	WSPWSSCTK	TCG	40

RESULT 13
US-08-313-288B-20
; Sequence 20, Application US/08313288B
; Patent No. 5750502
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M. and Avihu Klar

Query Match	77.9%;	Score 60;	DB 5;	Length 239;
Best Local Similarity	75.0%;	Pred. No. 2.8;		
Mismatches	0;	Mismatches	2;	Indels 0;
Conservative	0;	Conservative	0;	Gaps 0;

QY	1	WSGWSSCSRSCG	12
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RESULT 11
US-08-985-526-3
; Sequence 3, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutzz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington

; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
 ; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/313,288B
 ; FILING DATE: January 5, 1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 278-0400
 ; TELEFAX: (212) 391-0526
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1170 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-313-288B-20

Query Match 77.9%; Score 60; DB 1; Length 1170;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
 DB 385 WSEWTSCTSCG 396

RESULT 14
 US-09-657-472-2
 ; Sequence 2, Application US/09657472
 ; Patent No. 6727063
 ; GENERAL INFORMATION:
 ; APPLICANT: Lander, Eric S.
 ; APPLICANT: Cargill, Michele
 ; APPLICANT: Ireland, James S.
 ; APPLICANT: Bolik, Stacey
 ; APPLICANT: Daley, George Q.
 ; APPLICANT: McCarthy, Jeanette J.
 ; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
 ; FILE REFERENCE: 2825.1027-001
 ; CURRENT APPLICATION NUMBER: US/09/657,472
 ; CURRENT FILING DATE: 2000-09-07
 ; PRIOR APPLICATION NUMBER: US 60/153,357
 ; PRIOR FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: US 60/220,947
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: US 60/225,724
 ; PRIOR FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 2551
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1170
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-657-472-2

Query Match 77.9%; Score 60; DB 4; Length 1170;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
 DB 385 WSEWTSCTSCG 396

RESULT 15
 US-08-799-173A-12
 ; Sequence 12, Application US/08799173A
 ; Patent No. 5871969
 ; GENERAL INFORMATION:
 ; APPLICANT: HASTINGS, GREGG
 ; APPLICANT: PATRICK J. DILLON
 ; TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 ; STREET: 9410 KEY WEST AVENUE
 ; CITY: ROCKVILLE
 ; STATE: MD
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/799,173A
 ; FILING DATE: 11-FEB-1997
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROOKES, ANDERS A.
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF226
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 52 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-799-173A-12

Query Match 76.6%; Score 59; DB 2; Length 52;
 Best Local Similarity 66.7%; Pred. No. 1;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
 DB 6 WSEWTSCTSCG 17

Search completed: April 1, 2005, 14:01:57
 Job time: 21.1304 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:22:55 ; Search time 83.7391 Seconds
(without alignments)
55.424 Million cell updates/sec

Title: US-09-462-909D-8

Perfect score: 77

Sequence: 1 WSGWSSCSRSG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	77	100.0	12	2	AAW97445	Aw97445 Peptide t
2	68	88.3	606	8	ADP04709	Adp04709 Sea squir
3	68	88.3	4123	7	ABU62079	Abu62079 Human jel
4	68	88.3	4219	5	ADH48718	Adh48718 NOV1 prot
5	68	88.3	4561	4	ABG30203	Abg30203 Novel hum
6	68	88.3	5737	7	ADN95228	Adn95228 Human BEC
7	68	88.3	9222	4	ABG21064	Abg21064 Novel hum
8	65	84.4	997	4	AAW72283	Aaw72283 Human ADA
9	65	84.4	997	7	ADJ69288	Adj69288 Human hea
10	65	84.4	1054	4	ABE60410	Abb60410 Drosophil
11	65	84.4	1255	5	ADI28031	Adi28031 ECMCAD pr
12	65	84.4	1686	4	AAE00934	Aae00934 Human 278
13	65	84.4	1686	4	AAE00913	Aae00913 Human 278
14	65	84.4	1686	4	AAW74944	Aab74944 Human ADA
15	65	84.4	1686	8	ADJ58902	Adj58902 Human ADA
16	65	84.4	1690	4	AAW86949	Aab86949 Human met
17	65	84.4	1784	3	AAW41379	Aab41379 Human ORF
18	64	83.1	353	6	ABU19383	Abj19383 NOVX rela
19	64	83.1	353	8	ADO41766	Ado41766 Novel hum
20	63	81.8	556	5	ABG31503	Abg31503 Human ADA
21	63	81.8	571	6	ABR58452	Abr58452 Human NOV
22	63	81.8	577	6	ABR58460	Abr58460 Human NOV
23	63	81.8	722	6	ADA50469	Ada50469 Human pro
24	63	81.8	791	5	ABG76895	Abg76895 Human zin
25	63	81.8	791	7	ADJ38422	Adj38422 Human nov

26	63	81.8	856	5	ABG76896	Abg76896 Human ADA
27	63	81.8	856	7	ADJ38424	Adj38424 Human nov
28	63	81.8	928	8	ADR09503	Adr09503 Human pro
29	63	81.8	952	5	ABG76897	Abg76897 Human ADA
30	63	81.8	952	7	ADJ38426	Adj38426 Human nov
31	63	81.8	986	5	ABG76894	Abg76894 Human zin
32	63	81.8	986	7	ADJ38420	Adj38420 Human nov
33	63	81.8	1021	5	AAU79496	Aau79496 Human par
34	63	81.8	1072	6	ABR40093	Abr40093 Human ADA
35	63	81.8	1170	5	AAU79500	Aau79500 Human ADA
36	63	81.8	1224	5	AAU72891	Aau72891 Human met
37	63	81.8	1224	5	AAOL5254	Aao15254 Human MDT
38	63	81.8	1224	5	AAU79497	Aau79497 Human ADA
39	63	81.8	1224	5	AAU80153	Aau80153 Human ADA
40	63	81.8	1224	6	ABG72431	Abg72431 Novel hum
41	63	81.8	1224	6	ABR83432	Abr83432 Human ADA
42	63	81.8	1224	7	ADA50762	Ada50762 Novel hum
43	63	81.8	1224	8	ABM79745	Abm79745 Human pro
44	63	81.8	1236	5	AAU98886	Aau98886 Human pro
45	63	81.8	1237	8	ABM84501	Abm84501 Human dia

ALIGNMENTS

RESULT 1

AAW97445

ID AAW97445 standard; peptide; 12 AA.

XX AC AAW97445;

DT XX 19-MAY-1999 (first entry)

DE XX Peptide that is useful for regenerating the nervous system.

XX KW Neuronal sprouting; cerebral cortex; spinal cord cell; aggregation;

KW neurite defasculation; regeneration; nervous system cell;

KW neurodegeneration; Alzheimer's; Parkinson's disease; multiple sclerosis;

KW myopathy; synapse formation; neuroblastoma.

XX OS Synthetic.

XX PN WO9903890-A1.

XX PD 28-JAN-1999.

XX PF 16-JUL-1998; 98WO-FR001556.

XX PR 16-JUL-1997; 97FR-00009016.

XX PA (UYAU-) UNIV AUVERGNE.

XX PI Meinzel A, Monnerie H, Gobron S;

XX DR WPI; 1999-132166/11.

XX PT New polypeptides for promoting growth of neurons - useful for treatment of neurodegeneration, neuroblastoma and as additives for neuronal cell cultures.

XX PS Claim 6; Page 14; 29pp; French.

XX CC The present sequence represents a peptide that stimulates neuronal (particularly axonal) sprouting in neurons of the cerebral cortex, and in spinal cord cells inhibits aggregation and defasculation of neurites while increasing formation of synaptic contacts. The peptide is used to regenerate nervous system cells, particularly for treating neurodegeneration (e.g. Alzheimer's or Parkinson's diseases, multiple sclerosis and myopathy), other conditions requiring regeneration (particularly elongation and synapse formation) or neuroblastoma. The peptide can also be used as an additive for neuronal cell cultures

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 77; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
| | | | | | | |
DBD 1 WSGWSSCSRSCG 12

RESULT 2
ADP04709
IID ADP04709 standard; protein; 606 AA.
XX AC
XX ADP04709;
XX DT
XX 29-JUL-2004 (first entry)
DE Sea squirt protein with tissue specific expression in development Seq304.
XX sea squirt; regeneration medicine; gene therapy; cell proliferation;
KW differentiation; reproduction; environmental measurement; water survey.
XX OS Ciona intestinalis.
OS JP20040571129-A.
PN XX
PD XX
PP 26-FEB-2004.
PF 31-JUL-2002; 2002JP-00222593.
PR 31-JUL-2002; 2002JP-00222593.
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2004-287079/27.
DR N-PSDB; ADP04708.
XX Novel gene cluster which is specifically expressed in tissue or organ during developmental phase of sea squirt, useful for elucidation of mechanism of development of tissue or organ of sea squirt.

XX Claim 1; SEQ ID NO 304; 1846pp; Japanese.

XX This invention relates to novel genes and the encoded proteins thereof that are derived from the sea squirt Ciona intestinalis. Specifically, it refers to those genes that are expressed in the tissues or organs of the sea squirt during its developmental phase. The present invention describes the identification of these genes as useful for elucidation of the mechanism of development and hence for developing regeneration medicines and gene therapy techniques. Accordingly, they can be used in the research of various genetic diseases, as well as the analysis of cell proliferation, differentiation and reproduction. Furthermore, such compositions can be useful for environmental measurements and water surveys, particularly for sea water surveys, and also for the preparation of transformed sea squirt for improving edibility of sea squirt such as Halocynthia roretzi. This polypeptide sequence is a sea squirt protein sequence that has tissue specific expression during development, given in an exemplification of the invention.

XX SQ Sequence 606 AA;

Query Match 88.3%; Score 68; DB 8; Length 606;
Best Local Similarity 83.3%; Pred. No. 0.85;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
| : | | | | | | | |
Db 257 WTGWSSCSASCG 268

RESULT 3
ABUG62079

XX PD 06-SEP-2002.
 XX PF 26-FEB-2002; 2002WO-US005910.
 XX XX
 XX PR 26-FEB-2001; 2001US-0271646P.
 XX PR 27-FEB-2001; 2001US-0271840P.
 XX PR 28-FEB-2001; 2001US-0272404P.
 XX PR 28-FEB-2001; 2001US-0272405P.
 XX PR 28-FEB-2001; 2001US-0272410P.
 XX PR 28-FEB-2001; 2001US-0272414P.
 XX PR 02-MAR-2001; 2001US-0272787P.
 XX PR 02-MAR-2001; 2001US-0272922P.
 XX PR 02-MAR-2001; 2001US-0273048P.
 XX PR 02-MAR-2001; 2001US-0273000P.
 XX PR 16-MAR-2001; 2001US-0276401P.
 XX PR 20-MAR-2001; 2001US-0277324P.
 XX PR 20-MAR-2001; 2001US-0278660P.
 XX PR 30-MAR-2001; 2001US-0280039P.
 XX PR 30-MAR-2001; 2001US-0280234P.
 XX PR 02-APR-2001; 2001US-0280818P.
 XX PR 12-APR-2001; 2001US-0283443P.
 XX PR 23-APR-2001; 2001US-0285754P.
 XX PR 02-APR-2001; 2001US-0286096P.
 XX PR 03-MAY-2001; 2001US-0288353P.
 XX PR 17-MAY-2001; 2001US-0291703P.
 XX PR 31-MAY-2001; 2001US-0294834P.
 XX PR 20-JUN-2001; 2001US-0299695P.
 XX PR 21-JUN-2001; 2001US-0299845P.
 XX PR 05-JUL-2001; 2001US-0303242P.
 XX PR 13-AUG-2001; 2001US-0311981P.
 XX PR 16-AUG-2001; 2001US-0312858P.
 XX PR 17-AUG-2001; 2001US-0313280P.
 XX PR 29-AUG-2001; 2001US-0315614P.
 XX PR 17-SEP-2001; 2001US-0322818P.
 XX PR 25-FEB-2002; 2002US-00322818.
 XX PA

(CURA-) CURAGEN CORP.

XX PI Alsobrook JP, Anderson DW, Ballinger RA, Boldog FL, Burgess CE;
 PI Casman SV, Ellerman KE, Gangolli EA, Gerlach VL, Gilbert JA;
 PI Gorman L, Guo X, Gurev VY, Kekuda R, Li L, Liu X, Malyankar UM;
 PI Miller CB, Millet I, Padigaru M, Patturajan M, Pena CE, Peyman JA;
 PI Rastelli L, Shenoy SG, Shinkets RA, Smithson G, Spytek KA, Stone DU;
 PI Taupier RJ, Tchernev VT, Vernet CAM, Zerhusen BD;
 XX WPI; 2002-698672/75.
 DR N-PSDB; ADH48717.

XX PT New NOVX polypeptides or polynucleotides, useful for preventing or
 PT treating disorders or syndromes e.g., atherosclerosis, hypertension,
 PT obesity or cancer.

XX PS Claim 1; Page 13-14; 923pp; English.

XX CC The present invention relates to novel human NOVX proteins, where X is
 CC any number from 1 to 91 and their coding sequences. The proteins and
 CC coding sequences are useful for preventing or treating disorders or
 CC syndromes e.g. atherosclerosis, hypertension, obesity or cancer. NOV1 is
 CC a DJ075IH13.1 protein-like protein and its coding sequence maps to
 CC chromosome 8.

XX SQ Sequence 4219 AA;

Query Match 88.3%; Score 68; DB 5; Length 4219;
 Best Local Similarity 91.7%; Pred. No. 4.6;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
 ||| |||||
 Db 2614 WSWWSSCSRSCG 2625

RESULT 5
 ABG30203
 ID ABG30203 standard; protein; 4561 AA.
 XX AC ABG30203;
 XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #30194.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US008631.
 XX PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX Dmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS94390.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX PS Claim 20; SEQ ID NO 60562; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activities. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 4561 AA;

Query Match 88.3%; Score 68; DB 4; Length 4561;
 Best Local Similarity 91.7%; Pred. No. 5;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
 ||| |||||
 Db 1481 WSWWSSCSRSCG 1492

RESULT 6
 ADN95228

us-09-462-909d-8.rag

Fri Apr 1 15:03:05 2005

ADN95228 standard; protein; 5737 AA.
ADN95228;
01-JUL-2004 (first entry)
Human BEC/LEC-related protein sequence SeqID150.
growth; differentiation; blood endothelial cell; BEC;
lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
vasotrophic; antiinflammatory; gene therapy; endothelial cell disorder;
inflammatory disease; cancer metastasis; lymphatic system; human.
Homo sapiens.
WO2003080640-A1.
02-OCT-2003.
07-MAR-2003; 2003WO-US006900.
07-MAR-2002; 2002US-0363019P.
(LUDWIG) LUDWIG INST CANCER RES.
(LICN) LICENTIA LTD.
Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
WPI; 2003-876899/81.
N-PSDB; ADN95229.
Example 1; SEQ ID NO 150; 176pp; English.
This invention relates to a method of differentially modulating the
growth or differentiation of blood endothelial cells (BEC) or lymphatic
endothelial cells (LEC) comprising contacting endothelial cells with a
composition comprising an agent that differentially modulates blood or
lymphatic endothelial cells. Treating hereditary lymphoedema comprises
identifying a human subject with lymphoedema and with a mutation in at
least one allele of a gene encoding a LEC protein, where the mutation
correlates with lymphoedema in human subjects, and with the proviso that
the LEC protein is not VEGFR-3, and administering to the subject a
composition comprising a lymphatic growth agent selected from VEGF-C or
VEGF-D polypeptides and polynucleotides. The invention may be useful for
the development of compounds with an antiangiogenic, cytostatic,
vasotrophic or antiinflammatory activity or for gene therapy. The method
is useful in modulating the growth or differentiation of blood
endothelial cells or lymphatic endothelial cells, in treating hereditary
lymphoedema, in screening for an endothelial cell disorder or
predisposition to the disorder or in monitoring the efficacy or toxicity
of a drug on endothelial cells. The agent is useful in manufacturing a
medicament for the differential modulation of blood vessel endothelial
cell or lymphatic vessel endothelial cell growth or differentiation. The
lymphatic growth agent may also be used in manufacturing a medicament for
the treatment of hereditary lymphoedema resulting from a mutation in a
LEC gene or of other diseases involving the lymphatic vessels, such as
various inflammatory diseases and cancer metastasis via the lymphatic
system. The present sequence is that of a human LEC/BEC differentially
expressed protein which is related to the method of the invention. Note:
this sequence does not appear in the specification but was obtained by
the index using the source data given in table 14 of the specification.

Query Match 88.3%; Score 68; DB 7; Length 5737;
Best Local Similarity 91.7%; Pred. NO. 6.1;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WSGWSSCSRSCG 12
DB 3022 WSVWSSCSRSCG 3033

RESULT 7
ABG21064
ID ABG21064 standard; protein; 9222 AA.
XX AC ABG21064;
XX AC ABG21064;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #21055.
XX DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX KW
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS85251.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX Claim 20; SEQ ID NO 51423; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 9222 AA;
Query Match 88.3%; Score 68; DB 4; Length 9222;
Best Local Similarity 91.7%; Pred. NO. 9.2;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WSGWSSCSRSCG 12
DB 2205 WSVWSSCSRSCG 2215

RESULT 8

AAB72283
ID AAB72283 standard; protein; 997 AA.
AC AAB72283;
XX
XX
DT 14-MAY-2001 (first entry)
XX
XX
DE Human ADAMTS-7 amino acid sequence.
XX
XX
KW ADAMTS-N; disintegrin; metalloprotease; thrombospondin type I motif;
KW tumour cachexia; inflammation; dermatoparaxis; EDS-VIIC; angiogenesis;
KW Ehlers-Danlos syndrome type VIIC; articular cartilage erosion; human;
KW metastasis; embryogenesis; egg implantation; chromosome 15; ADAMTS-7.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200111074-A2.
XX
XX
PD 15-FEB-2001.
XX
XX
PF 03-AUG-2000; 2000WO-US021223.
XX
XX
PR 06-AUG-1999; 99US-00369364.
XX
XX
PA (CLEV-) CLEVELAND CLINIC FOUND.
PA (APTE/) APTE S S.
PA (HURS/) HURSKAINEN T L.
PA (HIRO/) HIROHATA S.
XX
XX
PI Apte SS, Hurskainen TL, Hirohata S;
XX
XX
DR WPI; 2001-159978/16.
DR N-PSDB; AAF63440.
XX
XX
PT Murine and human 'A Disintegrin-like And Metalloprotease domain with
PT Thrombospondin type I motifs' proteins and the nucleic acids encoding
PT them, useful for treating e.g. tumors, inflammation and arthritis.
XX
XX
PS Claim 15; Fig 4; 181pp; English.
XX
XX
CC This invention relates to murine and human ADAMTS-N (A disintegrin-like
CC and metalloprotease domain with thrombospondin type I motifs) proteins,
CC designated ADAMTS-5, 6, 7, 8, 9, 10 and R1. Also included in the
CC invention are cDNA sequences encoding the proteins, and antibodies
CC specific for the proteins. The nucleic acid sequences and proteins may be
CC used in the prevention, diagnosis and treatment of diseases associated
CC with inappropriate ADAMTS-N expression. Disorders that may be treated
CC using the nucleic acids, proteins and antibodies include, for example
CC tumour cachexia, inflammation, dermatoparaxis in cattle or Ehlers-Danlos
CC syndrome type VIIC (EDS-VIIC) in humans, erosion of articular cartilage
CC in arthritic (both inflammatory and non-inflammatory) disease.
CC angiogenesis, tumour growth and metastases, and they may also be used for
CC controlling embryogenesis and implantation of fertilised eggs. The
CC present sequence represents human ADAMTS-7. The human ADAMTS-7 gene is
CC located on chromosome 15
XX
XX
SQ Sequence 997 AA;
Query Match 84.4%; Score 65; DB 4; Length 997;
Best Local Similarity 83.3%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 WSGWSSCSRSCG 12
DB 544 WSAWSICSRSCG 555
RESULT 9
ID ADJ69288
XX ADJ69288 standard; protein; 997 AA.
AC ADJ69288;
XX

06-MAY-2004 (first entry)
Human heat mitochondrial protein as a therapeutic target SeqID1094.
mitochondrial; human; screening assay; diabetes mellitus;
Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
Homo sapiens.
WO2003087768-A2.
23-OCT-2003.
04-APR-2003; 2003WO-US010870.
12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
(MITO-) MITOKOR.
(BUCK-) BUCK INST AGE RES.
Chosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
Warnock DE;
WPI; 2003-845369/78.
Identifying a mitochondrial target for drug screening assays and for
treating diseases associated with altered mitochondrial function,
comprises detecting a modified polypeptide in a sample and correlating
with the disease.
Claim 1; SEQ ID NO 1094; 180pp; English.
This invention relates to novel mitochondrial targets that can be used
for therapeutic intervention in treating a disease associated with
altered mitochondrial function. Specifically, it refers to a method for
identifying proteins of the human heart mitochondrial proteome that are
useful for drug screening assays, as well as therapeutic targets. The
present invention describes a method for identifying such proteins that
can be used in the treatment of various diseases associated with altered
mitochondrial function including diabetes mellitus, Huntington's disease,
osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
compositions have neuroprotective, neurotropic, antidiabetic,
anticonvulsant, antiarthritic, osteopathic, ophthalmological and
cytostatic activities. This polypeptide sequence is a human heart
mitochondrial protein of the invention.
Sequence 997 AA;
Query Match 84.4%; Score 65; DB 7; Length 997;
Best Local Similarity 83.3%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 WSGWSSCSRSCG 12
DB 544 WSAWSICSRSCG 555
RESULT 10
ID ABB60410
XX ABB60410 standard; protein; 1054 AA.
AC ABB60410;
XX
XX
DT 26-MAR-2002 (first entry)

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XX DE Drosophila melanogaster polypeptide SEQ ID NO 8022.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX XX 23-MAR-2001; 2001WO-US009231.
 XX XX 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR N-PSDB; ABL04513.
 XX XX New isolated nucleic acid detection reagent for detecting 1000 or more
 XX PT genes from Drosophila and for elucidating cell signaling and cell-cell
 XX PT interactions.
 XX XX Disclosure; SEQ ID NO 8022; 21pp + Sequence Listing; English.
 XX PS
 XX XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABR57737-
 CC ABR72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 1054 AA;
 XX
 XX Query Match 84.4%; Score 65; DB 4; Length 1054;
 XX Best Local Similarity 83.3%; Pred. No. 3.3;
 XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WSGWSSCSRSCG 12
 DB 629 WSEWSECSRSCG 640
 RESULT 11
 ID ADI28031
 ID ADI28031 standard; protein; 1255 AA.
 XX AC ADI28031;
 XX DT 15-APR-2004 (first entry)
 XX DE ECMAD protein 55022490CD1.
 XX KW nootropic; antisickling; antianemic; antitumor; anti-HIV; anti-allergic;
 KW KW antianemic; antiaethmatic; immunosuppressive; antiatherosclerotic;
 KW KW dermatological; nephrotrophic; antigout; antithyroid; neuroprotective;
 KW KW osteopathic; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
 KW KW antiinflammatory; ophthalmological; anticonvulsant; antiparkinsonian;
 KW KW antibacterial; virucide; tranquilizer; neuroleptic; antidiabetic;
 KW KW cytostatic; hepatotrophic; gene therapy;
 KW KW human extracellular matrix and cell adhesion molecule; ECMCAD; diagnosis;
 KW KW genetic disorder; adrenoleukodystrophy; Down's syndrome; cystic fibrosis;
 KW KW Gaucher's disease; myotonic dystrophy; sickle cell anemia; thalassemia;
 KW KW Wilms' tumor; immunological disorder; acquired immunodeficiency syndrome;

KW AIDS; adult respiratory distress syndrome; allergy; anemia; asthma;
 KW KW atherosclerosis; autoimmune hemolytic anemia; contact dermatitis;
 KW KW Goodpasture's syndrome; gout; Grave's disease; multiple sclerosis;
 KW KW osteoporosis; psoriasis; rheumatoid arthritis; scleroderma;
 KW KW systemic lupus erythematosus; ulcerative colitis; uveitis;
 KW KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
 KW KW Huntington's disease; Parkinson's disease; multiple sclerosis;
 KW KW meningitis; periodic paralysis; mental disorder; mood; anxiety;
 KW KW schizophrenia; amnesia; diabetic neuropathy; connective tissue disorder;
 KW KW osteoporosis; Paget's disease; osteonecrosis; osteomyelitis;
 KW KW chondrosarcoma; giant cell tumor; psoriatic arthritis;
 KW KW infectious arthritis; systemic sclerosis; cell proliferative disorder;
 KW KW actinic keratosis; atherosclerosis; hepatitis; psoriasis; cancer;
 KW KW adenocarcinoma; leukemia; lymphoma; melanoma; myeloma.
 XX Homo sapiens.
 XX OS WO200202634-A2.
 XX PN 10-JAN-2002.
 XX PD 29-JUN-2001; 2001WO-US021067.
 XX PF 30-JUN-2000; 2000US-0215454P.
 XX PR 18-JUL-2000; 2000US-0219462P.
 XX PR 12-OCT-2000; 2000US-0240106P.
 XX PR 12-OCT-2000; 2000US-0240111P.
 XX PR 27-OCT-2000; 2000US-0244021P.
 XX PR 14-NOV-2000; 2000US-0248887P.
 XX PR 16-NOV-2000; 2000US-0249570P.
 XX (INCV-) INCVTE GENOMICS INC.
 XX PA Tang YT, Yue H, Azimzai Y, He A, Batra S, Lo TP, Nguyen DB;
 XX PI Burfill JD, Marcus CA, Zingler KA, Gandhi AR, Lal P, Kearney L;
 XX PI Burford N, Yao MG, Walia NK, Elliot VS, Patterson C, Khan FA;
 XX PI Baughn MR, Hafalia AJA, Policky JL, Au-Young J, Lu Y, Borowsky ML;
 XX PI Lu DAM, Ramkumar J, Yang J, Gururajan R, Warren BA, Gietzen K;
 XX PI Xu Y, Kallick DA, Lee EA, Thangavelu K, Delegeane AM, Lee S;
 XX WPI; 2002-154732/20.
 XX DR N-PSDB; ADI28067.
 XX Novel isolated human extracellular matrix and cell adhesion molecules
 XX useful for treating, preventing connective tissue disorder e.g.
 XX osteoporosis, Paget's disease, genetic disorder e.g. cystic fibrosis,
 XX thalassemia.
 XX Claim 1; SEQ ID NO 23; 270pp; English.
 XX The invention relates to a novel isolated human extracellular matrix and
 XX cell adhesion molecule (referred to as ECMCAD 1-36), its biologically to
 XX active or immunogenic fragment or a sequence comprising 90 % identity to
 XX ECMCAD 1-36. The molecule is useful for screening a compound for
 XX effectiveness as agonist or antagonist of itself. The protein and its
 XX encoding nucleic acid are useful in the diagnosis, treatment and
 XX prevention of genetic disorder such as adrenoleukodystrophy, Down's
 XX syndrome, cystic fibrosis, Gaucher's disease, myotonic dystrophy, sickle
 XX cell anemia, thalassemia, Wilms' tumor, etc., immunological disorders such
 XX as acquired immunodeficiency syndrome (AIDS), adult respiratory distress
 XX syndrome, allergies, anemia, asthma, atherosclerosis, autoimmune
 XX hemolytic anemia, contact dermatitis, Goodpasture's syndrome, gout,
 XX Grave's disease, multiple sclerosis, osteoporosis, psoriasis, rheumatoid
 XX arthritis, scleroderma, systemic lupus erythematosus, ulcerative colitis,
 XX uveitis, etc., a neurological disorder such as epilepsy, stroke,
 XX Alzheimer's disease, Huntington's disease, Parkinson's disease, multiple
 XX sclerosis, bacterial and viral meningitis, periodic paralysis, mental
 XX disorders including mood, anxiety, and schizophrenic disorders, amnesia,
 XX diabetic neuropathy, etc., connective tissue disorder such as
 XX osteoporosis, Paget's disease, osteonecrosis, osteomyelitis,
 XX chondrosarcoma, giant cell tumor, psoriatic arthritis, infectious
 XX arthritis, systemic sclerosis, etc., and a cell proliferative disorder
 XX such as actinic keratosis, atherosclerosis, hepatitis, psoriasis, cancers

CC including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, etc.
 CC This sequence represents one of the novel proteins.

XX
 SQ Sequence 1255 AA;

Query Match 84.4%; Score 65; DB 5; Length 1255;
 Best Local Similarity 83.3%; Pred. No. 3.9;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12

Db 113 WSAWSICSRSCG 124

RESULT 12

AAE00934

ID AAE00934 standard; protein; 1686 AA.

AC AAE00934;

XX 04-JUL-2001 (first entry)

DE Human 27875 ADAM-TS (a disintegrin and metalloproteinase).

XX Human; ADAM-TS; A Disintegrin And Metalloproteinase; antiinflammatory;
 KW angiogenesis; bronchial asthma; Goodpasture's syndrome; metastasis;
 KW heart failure; cardiac hypertrophy; chronic ischaemic heart disease;
 KW sickle cell disease nephropathy; urinary tract obstruction; haemostatic;
 KW skeletal muscle disorder; myocardial infarction; blood vessel disorder;
 KW hypertension; atherosclerosis; vasculitis; renal artery stenosis; mumps;
 KW gonorrhea; tuberculosis; syphilis; spermatocytic seminoma; osteoporosis;
 KW rhabdomyosarcoma; glomerulonephritis; bone disorder; Paget's disease;
 KW rickets; osteomalacia; Hodgkin's disease; gene therapy; antibacterial;
 KW cardiant; tumour; thymoma; vasotropic; cytostatic; virucide.

XX Homo sapiens.

OS Key Location/Qualifiers

FH Peptide 1..30

FT /label= Signal_peptide

FT Modified-site 6..8

FT /note= "Protein kinase C phosphorylation site"

FT Protein 31..1686

FT /label= Human_mature_27875_ADAM-TS_protein

FT Modified-site 55..60

FT /note= "N-myristoylation site"

FT Modified-site 73..75

FT /note= "Protein kinase C phosphorylation site"

FT Domain 78..93

FT /note= "Crystallins beta and gamma Greek key motif"

FT Modified-site 94..97

FT /note= "N-glycosylation site"

FT Modified-site 110..112

FT /note= "Protein kinase C phosphorylation site"

FT Modified-site 115..120

FT /note= "N-myristoylation site"

FT Modified-site 141..146

FT /note= "N-myristoylation site"

FT Modified-site 147..150

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FT Modified-site 159..162

FT /note= "Casein kinase II phosphorylation site"

FT Binding-site 195..197

FT /note= "Cell attachment sequence"

FT Modified-site 214..217

FT /note= "Casein kinase II phosphorylation site"

FT Modified-site 214..216

FT /note= "Protein kinase C phosphorylation site"

FT Domain 244..259

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FT Modified-site 313..315

FT /note= "Protein kinase C phosphorylation site"

FT Modified-site 342..345

FT Modified-site 342..344

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FT Modified-site 373..376

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FT Domain 539..545

FT /note= "Growth factor and cytokine metalloproteinase family signature 2 domain"

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FT /note= "N-myristoylation site"

FT Domain 541..592

FT /label= Disintegrin_domain

FT Domain 542..592

FT /label= Thrombospondin_domain

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FT /note= "N-myristoylation site"

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FT Modified-site 598..600

FT /note= "Protein kinase C phosphorylation site"

FT Modified-site 605..608

FT /note= "Casein kinase II phosphorylation site"

FT Modified-site 614..619

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FT Modified-site 667..672

FT /note= "N-myristoylation site"

FT Binding-site 687..692

FT /note= "Cytochrome C family heme-binding site"

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FT /note= "N-myristoylation site"

FT Modified-site 693..696

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FT Modified-site 703..706

FT /note= "Casein kinase II phosphorylation site"

FT Modified-site 716..721

FT /note= "N-myristoylation site"

FT Modified-site 740..747

FT /note= "Tyrosine kinase phosphorylation site"

FT Modified-site 765..770

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FT Domain 825..868

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FT Modified-site 901..903

FT /note= "Protein kinase C phosphorylation site"

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FT Domain 949..994

FT /label= Thrombospondin_domain

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FT /label= Thrombospondin_domain

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0											
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Db	544	WSAWSICSRSCG	555								
RESULT 13											
AAE00913											
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XX	AAE00913;										
DT	04-JUL-2001	(first entry)									
XX	Human	27875 ADAM-TS protein, alternative version.									
XX	Human	ADAM-TS; A Disintegrin And Metalloproteinase; antiinflammatory; angiogenesis; bronchial asthma; Goodpasture's syndrome; metastasis; heart failure; cardiac hypertrophy; chronic ischaemic heart disease; sickle cell disease nephropathy; urinary tract obstruction; haemostatic; skeletal muscle disorder; myocardial infarction; blood vessel disorder; hypertension; atherosclerosis; syphilis; spermatozoic semina; osteoporosis; gonorrhea; tuberculosis; glomerulonephritis; bone disorder; Paget's disease; rhabdomyosarcoma; glomerulonephritis; bone disease; gene therapy; antibacterial; rickets; osteomalacia; Hodgkin's disease; vasotrophic; cytostatic; virucide. cardiant; tumour; thymoma; vasotrophic; cytostatic; virucide.									
OS	Homo sapiens.										
XX	Key	Location/Qualifiers									
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Query Match 84.4%; Score 65; DB 4; Length 1686;
 Best Local Similarity 83.3%; Pred. NO. 5;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRCG 12
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 DB 544 WSAWSICSRSCG 555

Db 544 WSAWSICSRSCG 555

Search completed: April 1, 2005, 13:54:26
Job time : 85.7391 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 13:24:31 ; Search time 75.6522 Seconds
(without alignments)
81.226 Million cell updates

Title: US-09-462-909D-7
Perfect score: 62
Sequence: 1 WSXWSXCSXXCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 16123378

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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Database :      UniProt_03.*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length	%			
1	58	93.5	504	2	Q69HL7	Q69hl7 ciona intes	
2	58	93.5	369	2	Q86FQ3	Q86fpq3 cryptospori	
3	57	91.9	238	2	Q76510	Q76510 cryptospori	
4	57	91.9	257	2	Q966K7	Q966k7 caenorhabdi	
5	57	91.9	872	2	Q22580	Q22580 caenorhabdi	
6	57	91.9	1077	1	SM5A_MOUSE	Q62217 mus musculu	
7	57	91.9	1093	2	Q70C32	Q7qc32 anopheles g	
8	57	91.9	498	2	Q8CG65	Q8cg65 mus musculu	
9	57	91.9	541	2	Q700K0	Q700k0 rattus norv	
10	56	90.3	106	2	Q43982	Q43982 cryptospori	
11	56	90.3	156	2	Q8MXK6	Q8mxk6 cryptospori	
12	56	90.3	168	2	Q9GZ21	Q9gz21 cryptospori	
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16	56	90.3	449	2	Q8QFV1	Q8qfv1 xenopus lae	
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18	56	90.3	549	2	Q87988	Q87988 drosophila	
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21	56	90.3	654	2	Q19284	Q19284 caenorhabdi	
22	56	90.3	656	2	Q86FQ8	Q86fpq8 cryptospori	
23	56	90.3	660	2	Q23832	Q23832 cryptospori	
24	56	90.3	687	2	Q23729	Q23729 cryptospori	
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27	56	90.3	839	2	Q8ML26	Q8ml26 drosophila	
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29	56	90.3	880	2	Q8MSF8	Q8msf8 drosophila	
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RESULT 1

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ID Q69HL7 PRELIMINARY; PRT; 504 AA.

AC	Q69HL7;	25-OCT-2004	(TREMLrel. 28, Created)
DT		25-OCT-2004	(TREMLrel. 28, Last sequence update)
DT		25-OCT-2004	(TREMLrel. 28, Last annotation update)
DE	Htt-1-like		(Fragment).

OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI TaxID=7719;

RP SEQUENCE FROM N.A.

RX MEDLINE=23047825; PubMed=14686582;
RA Terajima D., Yamada S., Uchino R., Ikawa
RA Arai Y., Wang H.G., Satoh N., Satake M.;

RT "Identification and sequence of seventy-nine new transcripts expressed
RT in hemocytes of *Ciona intestinalis*, three of which may be involved in
RT characteristic cell-cell communication.";

RL DNA Res. 10:203-212 (2003).

DR EMBL; AY261898; AAP91764.1; -.
DR GO: GO:0005576: C:extracellular: IEA.

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DR  SO, 00000000, C:EXTRAORDINARY, I
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DR  InterPro; IPR0000345; CrtC hemo pg

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DR InterPro; IPR000345; CYTC_heme_BS
DR InterPro; IPR000884; TSP1.
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DR Pfam; PF00188; SCP; 1.

DR Pfam; PF00090; TSP_1; 4.
DR PRINTS: PR00838; V5ALLERGEN.

DR PRINTS; PR00837; V5TPXLIKE.
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DR PRINTS; PR00837; V5TPXLIKE.

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DR ProdM; PB000542; Allrgn_V5/tpx1;
DR SMART; SM00198; SCP; 1.
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DR SMART; SM00209; TSP1; 4.
DR PROSITE; PS01009; CRISP 1; 1.

DR PROSITE; PS01010; CRISP_2; UNKNOWN
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DR PROSITE; PS50092; TSP1; 5.

FT	NON_TER	I	I
FT	NON_TER	504	504

SQ SEQUENCE 504 AA; 55337 MW; 30

Query Match	93.5%	Score
Best Local Similarity	66.7%	Predicted

Best Local Similarity 88.7%; Free
Matches 8; Conservative 0; M

Qy 1 WSXWSXCXXCG 12

Db 477 WSAWSACSTSCG 488

100

RESULT 2

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ID	Q86PQ3	PRELIMINARY;
		PRT

Fri Apr 1 15:03:05 2005

AC Q86PQ3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE TSP1 domain-containing protein TSP2 precursor.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=22326344; PubMed=12438378;
RA DOI=10.1128/IAI.70.12.6987-6995.2002;
RA Deng M., Templeton T.J., London N.R., Bauer C., Schroeder A.A.,
RA Abrahamson M.S.;
RT "Cryptosporidium parvum genes containing thrombospondin type 1
domains";
RL Infect. Immun. 70:6987-6995(2002).
DR EMBL; AY190984; AAC039046.1; -;
DR HSP; P07996; ILSL.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR002086; Aldehyd_dehydrog.
DR InterPro; IPR000800; Notch_region.
DR InterPro; IPR003582; ShKT.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00066; Notch; 2.
DR Pfam; PF01549; ShKT; 5.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00090; TSP_1; 10.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00004; NL; 6.
DR SMART; SM00254; ShKT; 5.
DR SMART; SM00209; TSP1; 11.
DR PROSITE; PS00198; 4Fe4S FERREDOXIN; UNKNOWN 3.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS50092; TSP1; 10.
KW Signal.
FT SIGNAL
SQ SEQUENCE 366 AA; 429514 MW; 1F4851B7B0787B87 CRC64;
Query Match 93.5%; Score 58; DB 2; Length 3869;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 WSXWSXCSXCG 12
Db 386 WSSWSGSTSCG 397
RESULT 3
ID O76510 PRELIMINARY; PRT; 238 AA.
AC O76510;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thrombospondin-related adhesive protein (Fragment).
GN Name=TRAP-C3;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Moreduin;
RA Spano F., Putignani L., Crisanti A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF073838; AAC26812.1; -;
DR HSP; P07996; ILSL.
DR InterPro; IPR002086; Aldehyd_dehydrog.

DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP_1; 3.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS50092; TSP1; 3.
FT NON_TER 1
FT NON_TER 238
SQ SEQUENCE 238 AA; 26307 MW; 28242DE88F62C5A2 CRC64;
Query Match 91.9%; Score 57; DB 2; Length 238;
Best Local Similarity 66.7%; Pred. No. 0.35;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 WSXWSXCSXCG 12
Db 47 WSSWSACSXCG 58
RESULT 4
ID Q966K7 PRELIMINARY; PRT; 257 AA.
AC Q966K7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein F14H12.3.
GN Name=F14H12.3; ORFNames=F14H12.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nelson J., Gattung S., R Wilson.;
RT "The sequence of C. elegans cosmid F14H12.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006630; AAK68325.1; -;
DR HSP; P07996; ILSL.
DR WormBase; WBGene00017471; F14H12.3.

DA
KROGIEL, 199032, 1994, 9.
KW
Developmental protein; Multigene family; Neurogenesis;
Repeat; Signal; Transmembrane.
KW

FT	SIGNAL	1	21	Potential.	
FT	CHAIN	22	1077	Semaphorin 5A.	
FT	DOMAIN	22	971	Extracellular (Potential).	
FT	TRANSMEM	972	992	Potential.	
FT	DOMAIN	993	1077	Cytoplasmic (Potential).	
FT	DOMAIN	35	484	Sema.	
FT	DOMAIN	540	593	TSP type-1 1.	
FT	DOMAIN	595	651	TSP type-1 2.	
FT	DOMAIN	653	702	TSP type-1 3.	
FT	DOMAIN	707	765	TSP type-1 4.	
FT	DOMAIN	784	839	TSP type-1 5.	
FT	DOMAIN	841	896	TSP type-1 6.	
FT	DOMAIN	897	944	TSP type-1 7.	
FT	DOMAIN	104	114	By similarity.	
FT	DISULFID	131	140	By similarity.	
FT	DISULFID	278	320	By similarity.	
FT	DISULFID	487	504	By similarity.	
FT	DISULFID	496	513	By similarity.	
FT	CARBOHYD	147	147	N-linked (GLNAC. . .)	(Potential).
FT	CARBOHYD	168	168	N-linked (GLNAC. . .)	(Potential).
FT	CARBOHYD	227	227	N-linked (GLNAC. . .)	(Potential).
FT	CARBOHYD	277	277	N-linked (GLNAC. . .)	(Potential).
FT	CARBOHYD	323	323	N-linked (GLNAC. . .)	(Potential).
FT	CARBOHYD	367	367	N-linked (GLNAC. . .)	(Potential).
FT	CARBOHYD	536	536	N-linked (GLNAC. . .)	(Potential).
FT	CARBOHYD	591	591	N-linked (GLNAC. . .)	(Potential).
FT	CARBOHYD	717	717	N-linked (GLNAC. . .)	(Potential).
FT	CARBOHYD	933	933	N-linked (GLNAC. . .)	(Potential).
SQ	SEQUENCE	1077 AA;	120826 MW;	EDAB0DDA42789FF CRC64;	
Query Match 91.9%; Score 57; DB 1; Length 1077;					
Best Local Similarity 66.7%; Pred. No. 1.2;					
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;					
QY	1 WSKWSKCSXXCG 12				
Db	847 WSSWSKCSATCG 858				
RESULT 7					
ID	Q7QC32	PRELIMINARY;	PRT;	1093 AA.	
AC	Q7QC32;	2004 (TREMBlrel. 26, Created)			
DT	01-MAR-2004	(TREMBlrel. 26, Last sequence update)			
DT	01-MAR-2004	(TREMBlrel. 26, Last annotation update)			
DE	Ebi11179	(Fragment)			
CN	Name=ehiG1179;	ORFNames=ENSANGG0000001015;			
OS	Anopheles gambiae str. PEST.				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.				
OX	NCBI_TaxID=180454;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=PEST;				
RA	Anopheles Genome Sequencing Consortium;				
RL	Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.				
CC	-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.				
CC	EMBL; AAAB01008859; EAA07529.1; --				
DR	HSSP; Q92854; 10LZ.				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	GO; GO:0004872; F:receptor activity; IEA.				
DR	InterPro; IPR002165; Flexin_repeat.				
DR	InterPro; IPR001627; Sema.				
DR	InterPro; IPR000884; TSP1.				
DR	InterPro; IPR008085; TSP_1.				
DR	Pfam; PF01437; PSI; 1.				
DR	Pfam; PF01403; Sema; 1.				
DR	Pfam; PF00090; TSP 1; 5.				
DR	PRINTS; PR01705; TSP1REPEAT.				
DR	PROSITE; PS00092; TSP1; 5.				
Query Match 91.9%; Score 57; DB 1; Length 1077;					
Best Local Similarity 66.7%; Pred. No. 1.2;					
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;					
QY	1 WSKWSKCSXXCG 12				
Db	847 WSSWSKCSATCG 858				
RESULT 8					
ID	Q8CG65	PRELIMINARY;	PRT;	4998 AA.	
AC	Q8CG65;				
DT	01-MAR-2003	(TREMBlrel. 23, Created)			
DT	01-MAR-2003	(TREMBlrel. 23, Last sequence update)			
DT	01-MAR-2004	(TREMBlrel. 26, Last annotation update)			
DE	SCO-spondin.				
OS	Name=Scospondin; Synonyms=sco-spondin;				
GN	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ICR; TISSUE=Brain;				
RA	Goncalves N., Simon-Chazottes D., Creveaux I., Meinzel A.,				
RA	Guenet J.-L., Meinzel R.;				
RT	"Mouse SCO-spondin, a gene of the thrombospondin type 1 repeat (TSR)				
RT	superfamily expressed in the brain.";				
RL	Gene 312:263-270(2003)				
CC	-!- SIMILARITY: Contains 1 F5/8 type C domain.				
DR	EMBL; AJ491857; CAD42654.1; --				
DR	HSSP; P01130; 1AJJ.				
DR	MGD; MGI:2674311; Scospondin.				
DR	GO; GO:005737; C:cytoplasm; IC.				
DR	InterPro; IPR000923; BlueCu_1.				
DR	InterPro; IPR002919; Cyrich_TIL.				
DR	InterPro; IPR006207; Cys_knot_C.				
DR	InterPro; IPR006209; EGF_like.				
DR	InterPro; IPR011489; EMI.				
DR	InterPro; IPR000421; FAS8 C.				
DR	InterPro; IPR001545; Gly_hormoneB.				
DR	InterPro; IPR002172; LDL_receptor_A.				
DR	InterPro; IPR008037; Prot_inh_PMP.				
DR	InterPro; IPR000884; TSP1.				
DR	InterPro; IPR008085; TSP_1.				
DR	InterPro; IPR001007; VWF C.				
DR	InterPro; IPR001846; VWF_D.				
DR	Pfam; PF07546; EMI; 1.				
DR	Pfam; PF00754; F5_F8_type_C; 1.				
DR	Pfam; PF00057; Ldl_recept_a; 10.				
DR	Pfam; PF05375; Pacifastin_1; 1.				
DR	Pfam; PF01826; TIL; 10.				
DR	Pfam; PF00090; TSP 1; 25.				
DR	Pfam; PF00093; VWC; 1.				
DR	Pfam; PF00094; VWD; 2.				
DR	PRINTS; PR00261; LDLRECEPTOR.				
DR	PRINTS; PR01705; TSP1REPEAT.				
DR	SMART; SM00231; FAS8C; 1.				
DR	SMART; SM00068; GHB; 1.				
DR	SMART; SM00192; LDLA; 10.				
DR	SMART; SM00209; TSP1; 25.				
DR	SMART; SM00214; VWC; 4.				
DR	SMART; SM00216; VWD; 2.				
DR	PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.				
DR	PROSITE; PS01225; CTCK_2; 1.				
DR	PROSITE; PS01186; EGF_2; 2.				
DR	PROSITE; PS00022; FAS8C_3; 1.				
DR	PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_2.				


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DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS50068; LDLRA_2; 10.
DR PROSITE; PS50092; TSPI; 25.
DR PROSITE; PS01208; VWFC_1; UNKNOWN_1.
DR PROSITE; PS50184; VWFC_2; 2.
SQ SEQUENCE 4998 AA; 535028 MW; DA2ABA8DA47DF225 CRC64;

Query Match 91.9%; Score 57; DB 2; Length 4998;
Best Local Similarity 66.7%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 4012 WSAWSCHSCG 4023

RESULT 9
Q700K0 PRELIMINARY; PRT; 5141 AA.
AC Q700K0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SCO-spondin.
GN Name=sco-spondin;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Meinel O.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 F5/8 type C domain.
DR EMBL; AJ629845; CAP33425.1; -.
DR HSSP; P01130; IAJJ.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR002919; Cysrich TIL.
DR InterPro; IPR006207; Cys knot C.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011489; EMI.
DR InterPro; IPR000421; FAS8_C.
DR InterPro; IPR01545; Gly_hormoneB.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR006552; VWC_out.
DR InterPro; IPR01007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF07546; EMI; 1.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00057; Ldl_recept_a; 8.
DR Pfam; PF01826; TIL; 10.
DR Pfam; PF00090; TSP_1; 25.
DR Pfam; PF00093; VWC; 1.
DR Pfam; PF00094; VWD; 3.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00192; LDLa; 10.
DR SMART; SM00209; TSPI; 25.
DR SMART; SM00214; VWC; 5.
DR SMART; SM00215; VWC_out; 9.
DR SMART; SM00216; VMD; 3.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS50022; FASEC_3; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_2.
DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS50068; LDLRA_2; 10.
DR PROSITE; PS50092; TSPI; 24.
DR PROSITE; PS01208; VWFC_1; UNKNOWN_1.
DR PROSITE; PS0184; VWFC_2; 2.
SQ SEQUENCE 5141 AA; 550644 MW; 1772AE67F02CA5E3 CRC64;

Query Match 91.9%; Score 57; DB 2; Length 5141;

Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 4161 WSAWSCHSCG 4172

RESULT 10
Q43982 PRELIMINARY; PRT; 106 AA.
AC Q43982;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE TRAP-C1 (Fragment).
GN Name=TRAP-C1;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F12;
RX MEDLINE=98443215; PubMed=9769250; DOI=10.1006/expr.1998.4324;
RA Spano F., Putignani L., Guida S., Crisanti A.;
RT "Cryptosporidium parvum: PCR-RFLP analysis of the TRAP-C1
RT (thrombospondin-related adhesive protein of Cryptosporidium-1) gene
RT discriminates between two alleles differentially associated with
RT parasite isolates of animal and human origin.";
RL Exp. Parasitol. 90:195-198(1998).
DR EMBL; AF033828; AAB92609.1; -.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF00090; TSP_1; 1.
DR SMART; SM00209; TSPI; 2.
DR PROSITE; PS50092; TSPI; 2.
FT NON TER 1
FT NON TER 106
SQ SEQUENCE 106 AA; 11771 MW; 34D970D252058136 CRC64;

Query Match 90.3%; Score 56; DB 2; Length 106;
Best Local Similarity 66.7%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 72 WSEWSDCSTSCG 83

RESULT 11
Q8MXK6 PRELIMINARY; PRT; 156 AA.
AC Q8MXK6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Thrombospondin related adhesive protein (Fragment).
GN Name=TRAP-C1;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HNJ-1;
RA Sato M., Kimata I., Iseki M., Nakai Y.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB089293; BAC07243.1; -.
DR HSSP; P07996; 1LSL.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF00090; TSP_1; 1.
DR SMART; SM00209; TSPI; 2.
DR PROSITE; PS50092; TSPI; 2.
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Fri Apr 1 15:03:05 2005

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FT NON_TER 1
FT NON_TER 156
SQ SEQUENCE 156 AA; 17312 MW; 6439FFB1F221047E CRC64;

Query Match
Best Local Similarity 90.3%; Score 56; DB 2; Length 156;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 85 WSEWSDCSTSCG 96

RESULT 12
ID Q9GZ21 PRELIMINARY; PRT; 168 AA.
AC Q9GZ21, 2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Thrombospondin-related adhesive protein (Fragment).
GN Name=TRAP-C1;
OS Cryptosporidium meleagridis.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=93969;
[1]
SEQUENCE FROM N.A.
MEDLINE=20389602; PubMed=10930736;
Pedraza-Diaz S., Amar C., McLauchlin J.;
"The identification and characterisation of an unusual genotype of
Cryptosporidium from human faeces as Cryptosporidium meleagridis.";
FEMS Microbiol. Lett. 189:189-194 (2000).
DR EMBL; AF248746; AAG01095.1; -.
DR HSSP; P07996; 1LSL.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP_1; 2.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS50092; TSP1; 3.
FT NON_TER 1
FT NON_TER 168
SQ SEQUENCE 168 AA; 18576 MW; CE9516EE86479C3 CRC64;

Query Match
Best Local Similarity 90.3%; Score 56; DB 2; Length 168;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 85 WSEWSDCSTSCG 96

RESULT 13
ID Q9GZ22 PRELIMINARY; PRT; 168 AA.
AC Q9GZ22, 2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Thrombospondin-related adhesive protein (Fragment).
GN Name=TRAP-C1;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
[1]
SEQUENCE FROM N.A.
MEDLINE=20389602; PubMed=10930736;
Pedraza-Diaz S., Amar C., McLauchlin J.;
"The identification and characterisation of an unusual genotype of
Cryptosporidium from human faeces as Cryptosporidium meleagridis.";
FEMS Microbiol. Lett. 189:189-194 (2000).
DR EMBL; AF248745; AAG01094.1; -.

FT NON_TER 1
FT NON_TER 156
SQ SEQUENCE 156 AA; 17312 MW; 6439FFB1F221047E CRC64;

Query Match
Best Local Similarity 90.3%; Score 56; DB 2; Length 168;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 85 WSEWSDCSTSCG 96

RESULT 14
ID Q9GZ23 PRELIMINARY; PRT; 168 AA.
AC Q9GZ23, 2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Thrombospondin-related adhesive protein (Fragment).
GN Name=TRAP-C1;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
[1]
SEQUENCE FROM N.A.
MEDLINE=20389602; PubMed=10930736;
Pedraza-Diaz S., Amar C., McLauchlin J.;
"The identification and characterisation of an unusual genotype of
Cryptosporidium from human faeces as Cryptosporidium meleagridis.";
FEMS Microbiol. Lett. 189:189-194 (2000).
DR EMBL; AF248744; AAG01093.1; -.
DR HSSP; P07996; 1LSL.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP_1; 2.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS50092; TSP1; 3.
FT NON_TER 1
FT NON_TER 168
SQ SEQUENCE 168 AA; 18614 MW; F2AD32849A8B5E9C CRC64;

Query Match
Best Local Similarity 90.3%; Score 56; DB 2; Length 168;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 85 WSEWSDCSTSCG 96

RESULT 15
ID Q7JN23 PRELIMINARY; PRT; 192 AA.
AC Q7JN23, 2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE TRAP-C1 (Thrombospondin related adhesive protein) (Fragment).
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
[1]
SEQUENCE FROM N.A.
Spano F.S.;
Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RL
```

```

DR EMBL; X77587; CAA54690.1; -.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP_1; 2.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS50092; TSP1; 3.
FT NON_TER 1 192
FT NON_TER 192 192
SQ SEQUENCE 192 AA; 21229 MW; B90CF7BDA2579612 CRC64;

Query Match      90.3%; Score 56; DB 2; Length 192;
Best Local Similarity 66.7%; Pred. No. 0.42;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 WSXWSXCSXXCG 12
      |||||
Db      80 WSEWSDCSTSCG 91

Search completed: April 1, 2005, 13:59:21
Job time : 78.6522 secs

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:43:07 ; Search time 16.6957 Seconds
(without alignments)
69.156 Million cell updates/sec

Title: US-09-462-909D-7

Perfect score: 62

Sequence: 1 WSXWSXCSXXCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	91.9	860	T16892	hypothetical prote
2	56	90.3	654	T29247	hypothetical prote
3	56	90.3	724	A48569	antigen Em100 - Ei
4	56	90.3	984	T00326	hypothetical prote
5	56	90.3	1444	T18856	angiogenesis inhib
6	56	90.3	1522	T00028	brain-specific ang
7	56	90.3	2098	T18397	protein CTRP - mal
8	55	88.7	788	T25061	hypothetical prote
9	55	88.7	803	A47723	F-spondin precurs
10	55	88.7	807	A38152	F-spondin - rat
11	55	88.7	957	T15976	hypothetical prote
12	55	88.7	1170	TSHUP1	thrombospondin 1 p
13	55	88.7	1170	A40558	thrombospondin 1 p
14	55	88.7	1172	TSHUP2	thrombospondin 2 p
15	55	88.7	1172	A42587	thrombospondin 2 p
16	55	88.7	1178	A39804	thrombospondin pre
17	55	88.7	1184	T09484	cartilage intermed
18	55	88.7	1584	T00026	brain-specific ang
19	54	87.1	805	T34212	hypothetical prote
20	54	87.1	1572	T00027	brain-specific ang
21	53	85.5	206	A45517	coccidioides-relate
22	53	85.5	610	T16761	hypothetical prote
23	53	85.5	712	A45638	immunodominant mic
24	53	85.5	1074	JC5928	semaphorin F precu
25	52	83.9	1059	T22545	hypothetical prote
26	51	82.3	123	A49108	TRAP-C2 protein -
27	51	82.3	551	T16557	hypothetical prote
28	51	82.3	651	T19477	hypothetical prote
29	51	82.3	919	T32541	unc-5 protein - Ca

unc-5 protein, lon
hypothetical prote
thrombospondin-rel
sporozyote surface
hypothetical prote
hypothetical prote
hypothetical prote
properdin precursor
hypothetical prote
sporozyote surface
hypothetical prote
gene ADAMTS-1 prot
hypothetical prote
protein F11C7.2 [i
properdin - mouse

ALIGNMENTS

RESULT 1

T16892 hypothetical protein T19D2.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T16892

R:Bentley, D.

submitted to the EMBL Data Library, December 1995

A:Description: The sequence of C. elegans cosmid T19D2.

A:Reference number: Z18599

A:Accession: T16892

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-860 <BEN>

A:Cross-references: UNIPROT:Q22580; EMBL:U42846; NID:gl125809; PID:gl125810; PIDN:AAA836C

C:Genetics:

A:Gene: CBSP.T19D2.1

A:Introns: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 58;

Query Match 91.9%; Score 57; DB 2; Length 860;

Best Local Similarity 66.7%; Pred. NO. 0.21;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12

Db 831 WSXWSXCSXXCG 842

RESULT 2

T29247 hypothetical protein F09F9.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T29247

R:Minx, P.; Hawkins, J.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F09F9.

A:Reference number: Z20594

A:Accession: T29247

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-654 <MIN>

A:Cross-references: UNIPROT:Q19284; EMBL:U40958; PIDN:AAA81764.1; CBSP:F09F9.4

C:Genetics:

A:Gene: CBSP.F09F9.4

A:Introns: 89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1; 523/1; 558/2; 596/2

Query Match 90.3%; Score 56; DB 2; Length 654;

Best Local Similarity 66.7%; Pred. NO. 0.24;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12

A;Accession: T18397
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2098 <TRO>
A;Cross-references: UNIPROT:Q25757; EMBL:U34363; NID:G1098897; PID:G1098898; PIDN:AAC469

Query Match 90.3%; Score 56; DB 2; Length 2098;
Best Local Similarity 66.7%; Pred. No. 0.57;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
DB 1644 WSDWSSCSKTCG 1655

RESULT 8
T25061
hypothetical protein T21B6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A;Accession: T25061
R;Cottage, A.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19975
A;Accession: T25061
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-788 <WIL>
A;Cross-references: UNIPROT:Q22631; EMBL:Z68011; PIDN:CAA92014.1; GSPDB:GN00028; CESP:T2
A;Experimental source: clone T21B6
C;Genetics:
A;Gene: CESP:T21B6.3
A;Map position: X
A;Introns: 20/1; 47/1; 76/1; 152/1; 735/2; 754/2

Query Match 88.7%; Score 55; DB 2; Length 788;
Best Local Similarity 66.7%; Pred. No. 0.39;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
DB 461 WSDWSTCSCTCG 472

RESULT 9
A47723
F-spondin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A47723
R;Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A;Title: Ectopic neural expression of a floor plate marker in frog embryos injected with
A;Reference number: A47723; MUID:93376785; PMID:8367492
A;Accession: A47723
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-803 <RUI>
A;Cross-references: UNIPROT:P35447; GB:L09123; NID:G409244; PIDN:AAA19105.1; PID:G409245
C;Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;435-489/Domain: thrombospondin type 1 repeat homology <THR2>
F;607-662/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 88.7%; Score 55; DB 2; Length 803;
Best Local Similarity 66.7%; Pred. No. 0.4;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
DB 614 WSDWSDCSVTCG 625

RESULT 10

A38152
F-spondin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A;Accession: A38152
R;Klar, A.; Baldassare, M.; Jessell, T.M.
Cell 69, 95-110, 1992
A;Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secreted
A;Reference number: A38152; MUID:92208952; PMID:1555244
A;Accession: A38152
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-807 <KLA>
A;Cross-references: UNIPROT:P35446; GB:M88469; NID:G204176; PIDN:AAA41174.1; PID:G204177
A;Experimental source: embryo floor plate
A;Note: sequence extracted from NCBI backbone (NCBIN:90877, NCBIP:90878)
C;Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;441-495/Domain: thrombospondin type 1 repeat homology <THR2>
F;500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F;557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F;613-666/Domain: thrombospondin type 1 repeat homology <THR1>
F;667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F;753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 88.7%; Score 55; DB 2; Length 807;
Best Local Similarity 66.7%; Pred. No. 0.4;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
DB 620 WSEWSDCSVTCG 631

RESULT 11
T15976
hypothetical protein F08C6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
A;Accession: T15976
R;Bentley, D.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F08C6.
A;Reference number: Z18440
A;Accession: T15976
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-957 <BEN>
A;Cross-references: UNIPROT:Q19204; EMBL:U29378; NID:G868184; PID:G868185; PIDN:AAA68721
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F08C6.1
A;Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3; 461/2; 498/3; 532/3; 627/2; 714/1; 715/1

Query Match 88.7%; Score 55; DB 2; Length 957;
Best Local Similarity 66.7%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
DB 858 WSGWSQCSVSCG 869

RESULT 12
TSHU1
thrombospondin 1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 23-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
A;Accession: A26155; A34274; A30140; A25812; A05172; A42927
R;Lawler, J.; Hynes, R.O.
J. Cell Biol. 103, 1635-1648, 1986
A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple ca
A;Reference number: A26155; MUID:87057617; PMID:2430973
A;Accession: A26155

A:Molecule type: mRNA
A:Residues: 1-1170 <LAH>
A:Cross-references: UNIPROT:P07986; GB:X04665; NID:G37137; PIDN:CAA28370.1; PID:G37138
A>Note: parts of this sequence, including the amino end of the mature protein, were determined by R.Laherty, C.D.; Giernan, T.M.; Dixit, V.M.
J. Biol. Chem. 264, 11222-11227, 1989
A:Title: Characterization of the promoter region of the human thrombospondin gene. DNA and protein
A:Reference number: A34274; MUID:89291870; PMID:2544587
A:Accession: A34274
A:Molecule type: DNA
A:Residues: 1-166 <LAH>
A:Cross-references: GB:J04835
R:Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, J. Cell Biol. 108, 729-736, 1989
A:Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the 5' noncoding region
A:Reference number: A30140; MUID:89139590; PMID:2918029
A:Accession: A30140
A:Molecule type: mRNA
A:Residues: 1-83, 'A', 85-522, 'A', 524-1170 <HEN>
A:Cross-references: EMBL:X14787; NID:G37464; PIDN:CAA32089.1; PID:G37465
A>Note: parts of this sequence, including the amino end of the mature protein, were determined by R.Kobayashi, S.; Eden-McCutchan, P.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A:Title: Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA
A:Reference number: A25812; MUID:87157592; PMID:3030396
A:Accession: A25812
A:Molecule type: mRNA
A:Residues: 1-83, 'A', 85-397 <KOB>
A:Cross-references: GB:M25631; NID:G538353; PIDN:AAA36741.1; PID:G538354
R:Dixit, V.M.; Hennessey, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
A:Reference number: A05172; MUID:86287276; PMID:3461443
A:Accession: A05172
A:Molecule type: mRNA
A:Residues: 1-83, 'A', 85-374, 'RC' <DIX>
A:Cross-references: GB:M14326; NID:G340005; PIDN:AAA61237.1; PID:G553801
A>Note: parts of this sequence, including the amino end of the mature protein, were determined by R.Sun, X.; Skorstengard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A:Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A:Reference number: A42927; MUID:92348511; PMID:1379247
A:Accession: A42927
A:Molecule type: Protein
A:Residues: 987-1003 <SUN>
A>Note: Cys-992 is shown to have a free sulfhydryl
C:Genetics:
A:Gene: GDB:THBS1; TSP1; TSP
A:Cross-references: GDB:I20438; OMIM:188060
A:Map position: 15q15-15q15
A:Introns: 23/1
A:Note: the list of introns may be incomplete
C:Complex: homotrimer, disulfide linked
C:Function:
A:Description: participates in cell migration and adhesion, and in platelet aggregation
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology; calcium binding; cell adhesion; glycoprotein; trimer
C:Keywords: beta-hydroxyasparagine; thrombospondin type 1 repeat homology <THR1>
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-1170/Product: thrombospondin 1 #status predicted <MAT>
F:317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F:378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F:434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F:491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F:551-586/Domain: EGF homology <EGF1>
F:551-586/Domain: EGF homology <EGF2>
F:650-689/Domain: EGF homology <EGF3>
F:926-928/Region: cell attachment (R-G-D) motif
F:171-232/Disulfide bonds: #status predicted
F:248,360,708,1067/Binding site: carboxyhydate (Asn) (covalent) #status predicted
F:270,274/disulfide bonds: interchain #status predicted
F:610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:1051/Binding site: carbohydrate (Asn) (covalent) #status absent

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 WSWXSCSXKCG 12
DB 441 WSPWSSCSVTCG 452
RESULT 13
A:0558
thrombospondin 1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1992 #sequence revision 05-Jun-1992 #text_change 09-Jul-2004
C:Accession: A40558; A37905; B42587; S68787
R:Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A. Genomics 11, 587-600, 1991
A:Title: Characterization of the murine thrombospondin gene.
A:Reference number: A40558; MUID:92128941; PMID:1774063
A:Accession: A40558
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1170 <LAH>
A:Cross-references: UNIPROT:P35441; GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M62453; GB:M62464; GB:M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:G51181
R:Bornstein, P.; Alfai, D.; Devarayalu, S.; Framson, P.; Li, P. J. Biol. Chem. 265, 16691-16698, 1990
A:Title: Characterization of the mouse thrombospondin gene and evaluation of the role of the 5' noncoding region
A:Reference number: A37905; MUID:90375546; PMID:2398070
A:Accession: A37905
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <BOR>
A:Cross-references: GB:J05605; GB:J05606; NID:G201991; PIDN:AAA40431.1; PID:G554390
R:Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seidlin, M.F.; Dixit, V.M. J. Biol. Chem. 267, 3274-3281, 1992
A:Title: Characterization of mouse thrombospondin 2 sequence and expression during cell differentiation
A:Reference number: A42587; MUID:92147683; PMID:1371115
A:Accession: B42587
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1152, 'P', 1154-1170 <LAH>
A:Cross-references: GB:M87276
A:Note: sequence extracted from NCBI backbone (NCBIP:81501)
R:Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F. FEBS Lett. 387, 36-41, 1996
A:Title: Expression and initial characterization of recombinant mouse thrombospondin 1 and 2
A:Reference number: S68787; MUID:96234006; PMID:8654563
A:Accession: S68787
A:Molecule type: protein
A:Residues: 19-26, 'X', 28-37 <CHE>
C:Complex: homotrimer, disulfide linked
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology; glycoprotein; homotrimer
C:Keywords: calcium binding; glycoprotein; #status predicted <SIG>
F:1-18/Domain: signal sequence #status predicted <MAT>
F:19-1170/Product: thrombospondin 1 #status predicted <MAT>
F:317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F:378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F:434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F:491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F:551-586/Domain: EGF homology <EGF>
F:248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 88.7%; Score 55; DB 2; Length 1170;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 WSWXSCSXKCG 12
DB 441 WSPWSSCSVTCG 452
RESULT 14
TSHUP2
thrombospondin 2 precursor - human

C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A47379; A42173
R;LaBell, T.L.; Byers, P.H.
Genomics 17, 225-229, 1993
A;Title: Sequence and characterization of the complete human thrombospondin 2 cDNA: pote
A;Reference number: A47379; MUID:94010892; PMID:8406456
A;Accession: A47379
A;Molecule type: mRNA
A;Residues: 1-1172 <LAB>
A;Cross-references: UNIPROT:P35442; GB:L12350; NID:G307505; PIDN:AAA03703.1; PID:G307506
R;LaBell, T.L.; Milewicz, D.J.; Distche, C.M.; Byers, P.H.
Genomics 12, 421-429, 1992
A;Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression c
A;Reference number: A42173; MUID:92217961; PMID:1559694
A;Accession: A42173
A;Molecule type: mRNA
A;Residues: 560-1172 <LA2>
A;Cross-references: GB:M81339
A;Experimental source: fibroblast
A;Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
C;Genetics:
A;Gene: GDB:THBS2; TSP2
A;Cross-references: GDB:128789; OMIM:188061
A;Map position: 6q27-6q27
C;Complex: homotrimer, disulfide linked
C;Function:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trim
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1172/Product: thrombospondin 2 #status predicted <MAT>
F;319-377/Domain: von Willebrand factor type C repeat homology <VWC>
F;380-431/Domain: thrombospondin type 1 repeat homology <THRI>
F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
F;553-588/Domain: EGF homology <EGF1>
F;652-691/Domain: EGF homology <EGF>
F;928-930/Region: cell attachment (R-G-D) motif
F;151.316.330.457.584.710.1069/Binding site: carbohydrate (Asn) (covalent) #status predi
F;167-226/Disulfide bonds: #status predicted
F;286,270/Disulfide bonds: interchain #status predicted
F;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 88.7%; Score 55; DB 1; Length 1172;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WSXWSXCSXCG 12
||| ||| |||
Db 443 WSPWSCSVTCG 454

RESULT 15
A42587
thrombospondin 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42587; A39851
R;Lahterty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M. .
J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: A42587
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-1172 <LAH>
A;Cross-references: UNIPROT:Q03350; GB:L07803; GB:M87275; NID:G340421; PIDN:AAA53064.1;
A;Note: sequence extracted from NCBI backbone (NCBIP:81502)
R;Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.
J. Biol. Chem. 266, 12821-12824, 1991
A;Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.
A;Reference number: A39851; MUID:91302287; PMID:1712771

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:59:39 ; Search time 61.8261 Seconds
(without alignments)
64.360 Million cell updates/sec

Title: US-09-462-909D-7

Perfect score: 62

Sequence: 1 WSXWSXCSXXC 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	91.9	1077	15 US-10-190-115-43	Sequence 43, Appl
2	57	91.9	1077	15 US-10-369-072-43	Sequence 43, Appl
3	56	90.3	52	15 US-10-019-065A-21	Sequence 21, Appl
4	56	90.3	660	11 US-09-939-853A-96	Sequence 96, Appl
5	56	90.3	997	9 US-09-918-171A-7	Sequence 7, Appl
6	56	90.3	997	10 US-09-981-151A-32	Sequence 32, Appl
7	56	90.3	997	16 US-10-408-765A-1094	Sequence 1094, Ap
8	56	90.3	1255	15 US-10-312-352-23	Sequence 23, Appl
9	56	90.3	1522	14 US-10-225-567A-346	Sequence 346, Appl
10	56	90.3	1886	15 US-10-386-414-2	Sequence 2, Appl
11	56	90.3	1690	9 US-09-788-043C-5	Sequence 5, Appl
12	56	90.3	4123	14 US-10-213-509-5	Sequence 5, Appl
13	56	90.3	4219	15 US-10-085-198-2	Sequence 2, Appl

14	88.7	23	14	US-10-042-696-12	Sequence 12, Appl
15	88.7	41	15	US-10-074-978A-408	Sequence 408, App
16	88.7	42	15	US-10-074-978A-406	Sequence 406, App
17	88.7	53	15	US-10-019-065A-13	Sequence 13, Appl
18	88.7	53	15	US-10-019-065A-14	Sequence 14, Appl
19	88.7	55	15	US-10-019-065A-7	Sequence 7, Appl
20	88.7	55	15	US-10-019-065A-10	Sequence 10, Appl
21	88.7	55	17	US-10-883-144-41	Sequence 41, Appl
22	88.7	56	17	US-10-883-144-36	Sequence 36, Appl
23	88.7	57	9	US-09-802-094-5	Sequence 5, Appl
24	88.7	57	9	US-09-802-094-6	Sequence 6, Appl
25	88.7	57	10	US-09-373-658-7	Sequence 7, Appl
26	88.7	57	10	US-09-373-658-10	Sequence 10, Appl
27	88.7	57	11	US-09-989-687-7	Sequence 7, Appl
28	88.7	57	11	US-09-989-687-10	Sequence 10, Appl
29	88.7	58	16	US-10-296-733-21	Sequence 21, Appl
30	88.7	61	16	US-10-296-733-23	Sequence 23, Appl
31	88.7	63	16	US-10-296-733-22	Sequence 22, Appl
32	88.7	170	15	US-10-419-462-43	Sequence 43, Appl
33	88.7	170	16	US-10-296-733-20	Sequence 20, Appl
34	88.7	170	16	US-10-296-733-25	Sequence 25, Appl
35	88.7	170	16	US-10-296-733-27	Sequence 27, Appl
36	88.7	170	17	US-10-782-968-43	Sequence 43, Appl
37	88.7	185	9	US-09-867-550-1306	Sequence 1306, Ap
38	88.7	194	15	US-10-019-065A-32	Sequence 32, Appl
39	88.7	218	13	US-10-036-869-1	Sequence 1, Appl
40	88.7	242	9	US-09-919-603-5	Sequence 5, Appl
41	88.7	246	15	US-10-296-115-977	Sequence 977, App
42	88.7	300	9	US-09-919-603-7	Sequence 7, Appl
43	88.7	311	9	US-09-863-824-6	Sequence 6, Appl
44	88.7	349	15	US-10-161-493-126	Sequence 126, App
45	88.7	353	15	US-10-161-493-128	Sequence 128, App

ALIGNMENTS

RESULT 1

US-10-190-115-43
; Sequence 43, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zernhusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01

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; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 43
; LENGTH: 1077
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-43

Query Match          91.9%; Score 57; DB 15; Length 1077;
Best Local Similarity 66.7%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 WSWXSCSXKCG 12
Db      847 WSSWSKCSATCG 858

RESULT 2
US-10-369-072-43
; Sequence 43, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grosse, William M
; APPLICANT: Szerkeres, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimketa, Richard
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586

QY      1 WSWXSCSXKCG 12
Db      847 WSSWSKCSATCG 858

US-10-019-065A-21
; Sequence 21, Application US/10019065A
; Publication No. US20040086501A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Corporation
; TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
; FILE REFERENCE: MSB-7265-PCT
; CURRENT APPLICATION NUMBER: US/10/019,065A
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/266,300
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Isolated type 1 thrombospondin domain sequence
US-10-019-065A-21

Query Match          90.3%; Score 56; DB 15; Length 52;
Best Local Similarity 66.7%; Pred. No. 0.97;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 WSWXSCSXKCG 12
Db      6 WSWMSTCSVTCG 17

RESULT 4
US-09-939-853A-96
; Sequence 96, Application US/09939853A
; Publication No. US20040039163A1
; GENERAL INFORMATION:
; APPLICANT: Burgess et al.
; TITLE OF INVENTION: No. US20040039163A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-099
; CURRENT APPLICATION NUMBER: US/09/939,853A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/228,191
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/267,300
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/269,961
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/277,337
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; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; PRIOR FILING DATE: 2000-07-17
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 1077
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-369-072-43

Query Match          91.9%; Score 57; DB 15; Length 1077;
Best Local Similarity 66.7%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 WSWXSCSXKCG 12
Db      847 WSSWSKCSATCG 858

RESULT 3
US-10-019-065A-21
; Sequence 21, Application US/10019065A
; Publication No. US20040086501A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Corporation
; TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
; FILE REFERENCE: MSB-7265-PCT
; CURRENT APPLICATION NUMBER: US/10/019,065A
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/266,300
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Isolated type 1 thrombospondin domain sequence
US-10-019-065A-21

Query Match          90.3%; Score 56; DB 15; Length 52;
Best Local Similarity 66.7%; Pred. No. 0.97;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 WSWXSCSXKCG 12
Db      6 WSWMSTCSVTCG 17

RESULT 4
US-09-939-853A-96
; Sequence 96, Application US/09939853A
; Publication No. US20040039163A1
; GENERAL INFORMATION:
; APPLICANT: Burgess et al.
; TITLE OF INVENTION: No. US20040039163A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-099
; CURRENT APPLICATION NUMBER: US/09/939,853A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/228,191
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/267,300
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/269,961
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/277,337
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; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Cryptosporidium wrairi
US-09-939-853A-96

Query Match 90.3%; Score 56; DB 11; Length 660;
Best Local Similarity 66.7%; Pred. No. 6.1;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSWXSCSXSCG 12
DB 352 WSEWSDCSTSCG 363

RESULT 5

US-09-918-171A-7
; Sequence 7, Application US/09918171A
; Patent No. US20020110894A1
; GENERAL INFORMATION:
; APPLICANT: Aptec, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/04193
; CURRENT APPLICATION NUMBER: US/09/918,171A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/369,364
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-7
US-09-918-171A-7

Query Match 90.3%; Score 56; DB 9; Length 997;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSWXSCSXSCG 12
DB 544 WSAWSICSRSCG 555

RESULT 6

US-09-981-151A-32
; Sequence 32, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkete, Richard A
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A

; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-151A-32

Query Match 90.3%; Score 56; DB 10; Length 997;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSWXSCSXSCG 12
DB 544 WSAWSICSRSCG 555

RESULT 7

US-10-408-765A-1094
; Sequence 1094, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 1077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1094
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1094

Query Match 90.3%; Score 56; DB 16; Length 997;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Publication No. US20030113798A1
/ GENERAL INFORMATION:
/ APPLICANT: LifeSpan Biosciences
/ APPLICANT: Brown, Joseph P.
/ APPLICANT: Burmer, Glenn C.
/ APPLICANT: Roush, Christine L.
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN
/ FILE REFERENCE: 1920-4-4
/ CURRENT APPLICATION NUMBER: US/10/225,567A
/ CURRENT FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 60/257,144
/ PRIOR FILING DATE: 2000-12-19
/ NUMBER OF SEQ ID NOS: 2292
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 346
/ LENGTH: 1522
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-225-567A-346

Query Match 90.3%; Score 56; DB 14; Length 1522;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 4; Indels 0;

QY 1 WSKWSKCSXXCG 12
Db 297 WSKWSKCSXXCG 308

RESULT 10
US-10-386-414-2
/ Sequence 2, Application US/10386414
/ Publication No. US20040006016A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapeller-Libermann, Rosana
/ APPLICANT: Robison, Keith E.
/ APPLICANT: White, David
/ APPLICANT: Williamson, Mark W.
/ APPLICANT: Cook, William James
/ APPLICANT: Meyers, Rachel E.
/ APPLICANT: MacBeth, Kyle J.
/ APPLICANT: Carroll, Joseph M.
/ APPLICANT: Chun, Miyoung
/ TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
/ FILE REFERENCE: MPI03-0210WNIM
/ CURRENT APPLICATION NUMBER: US/10/386,414
/ CURRENT FILING DATE: 2003-03-11
/ PRIOR APPLICATION NUMBER: 09/426,282
/ PRIOR FILING DATE: 1999-10-25
/ PRIOR APPLICATION NUMBER: 09/668,266
/ PRIOR FILING DATE: 2000-09-22
/ PRIOR APPLICATION NUMBER: 09/330,970
/ PRIOR FILING DATE: 1999-06-11
/ PRIOR APPLICATION NUMBER: 09/724,599
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: 09/860,193
/ PRIOR FILING DATE: 2001-05-16
/ PRIOR APPLICATION NUMBER: 10/283,023
/ PRIOR FILING DATE: 2002-10-29
/ PRIOR APPLICATION NUMBER: 60/335,044
/ PRIOR FILING DATE: 2001-10-31
/ PRIOR APPLICATION NUMBER: 10/010,943
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: 60/254,037
/ PRIOR FILING DATE: 2000-12-07
/ PRIOR APPLICATION NUMBER: 09/833,082
/ PRIOR FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 1686
/ TYPE: PRT

Publication No. US20030113798A1
/ GENERAL INFORMATION:
/ APPLICANT: LifeSpan Biosciences
/ APPLICANT: Brown, Joseph P.
/ APPLICANT: Burmer, Glenn C.
/ APPLICANT: Roush, Christine L.
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN
/ FILE REFERENCE: 1920-4-4
/ CURRENT APPLICATION NUMBER: US/10/225,567A
/ CURRENT FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 60/257,144
/ PRIOR FILING DATE: 2000-12-19
/ NUMBER OF SEQ ID NOS: 2292
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 346
/ LENGTH: 1522
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-225-567A-346

Query Match 90.3%; Score 56; DB 14; Length 1522;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 4; Indels 0;

QY 1 WSKWSKCSXXCG 12
Db 297 WSKWSKCSXXCG 308

RESULT 10
US-10-386-414-2
/ Sequence 2, Application US/10386414
/ Publication No. US20040006016A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapeller-Libermann, Rosana
/ APPLICANT: Robison, Keith E.
/ APPLICANT: White, David
/ APPLICANT: Williamson, Mark W.
/ APPLICANT: Cook, William James
/ APPLICANT: Meyers, Rachel E.
/ APPLICANT: MacBeth, Kyle J.
/ APPLICANT: Carroll, Joseph M.
/ APPLICANT: Chun, Miyoung
/ TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
/ FILE REFERENCE: MPI03-0210WNIM
/ CURRENT APPLICATION NUMBER: US/10/386,414
/ CURRENT FILING DATE: 2003-03-11
/ PRIOR APPLICATION NUMBER: 09/426,282
/ PRIOR FILING DATE: 1999-10-25
/ PRIOR APPLICATION NUMBER: 09/668,266
/ PRIOR FILING DATE: 2000-09-22
/ PRIOR APPLICATION NUMBER: 09/330,970
/ PRIOR FILING DATE: 1999-06-11
/ PRIOR APPLICATION NUMBER: 09/724,599
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: 09/860,193
/ PRIOR FILING DATE: 2001-05-16
/ PRIOR APPLICATION NUMBER: 10/283,023
/ PRIOR FILING DATE: 2002-10-29
/ PRIOR APPLICATION NUMBER: 60/335,044
/ PRIOR FILING DATE: 2001-10-31
/ PRIOR APPLICATION NUMBER: 10/010,943
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: 60/254,037
/ PRIOR FILING DATE: 2000-12-07
/ PRIOR APPLICATION NUMBER: 09/833,082
/ PRIOR FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 1686
/ TYPE: PRT

Publication No. US20030113798A1
/ GENERAL INFORMATION:
/ APPLICANT: LifeSpan Biosciences
/ APPLICANT: Brown, Joseph P.
/ APPLICANT: Burmer, Glenn C.
/ APPLICANT: Roush, Christine L.
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN
/ FILE REFERENCE: 1920-4-4
/ CURRENT APPLICATION NUMBER: US/10/225,567A
/ CURRENT FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 60/257,144
/ PRIOR FILING DATE: 2000-12-19
/ NUMBER OF SEQ ID NOS: 2292
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 346
/ LENGTH: 1522
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-225-567A-346

Query Match 90.3%; Score 56; DB 15; Length 1255;
Best Local Similarity 66.7%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSKWSKCSXXCG 12
Db 113 WSKWSKCSXXCG 124

RESULT 9
US-10-225-567A-346
/ Sequence 23, Application US/10312352
/ Publication No. US20040053824A1
/ GENERAL INFORMATION:
/ APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
/ APPLICANT: YOE, Henry; AZIMZAI, Yalda
/ APPLICANT: HE, Ann; BATRA, Sajeev
/ APPLICANT: LO, Terence P.; NGUYEN, Danniell B.
/ APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
/ APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.
/ APPLICANT: LAL, Preeti G.; KEARNEY, Liam
/ APPLICANT: BURFORD, Neil; YAO, Monique G.
/ APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.
/ APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.
/ APPLICANT: BAUGHN, Mariah R.; HAPALIA, April, J.A.
/ APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
/ APPLICANT: LU, Yan; BOROWSKY, Mark L.
/ APPLICANT: LU, Dyrng Aina M.; RAMKUMAR, Jayalaxmi
/ APPLICANT: YANG, Junming; GURURAJAN, Rajagopal
/ APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.
/ APPLICANT: XU, Yuming; KALLICK, Deborah A.
/ APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha
/ APPLICANT: DELEGEANE, Angelo M.; LEE, Sally
/ TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
/ FILE REFERENCE: PF-0794 USN
/ CURRENT APPLICATION NUMBER: US/10/312,352
/ CURRENT FILING DATE: 2002-12-18
/ PRIOR APPLICATION NUMBER: PCT/US01/21067
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: US 60/215,454
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 60/219,462
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: US 60/240,111
/ PRIOR FILING DATE: 2000-10-12
/ PRIOR APPLICATION NUMBER: US 60/240,106
/ PRIOR FILING DATE: 2000-10-12
/ PRIOR APPLICATION NUMBER: US 60/244,021
/ PRIOR FILING DATE: 2000-10-27
/ PRIOR APPLICATION NUMBER: US 60/248,887
/ PRIOR FILING DATE: 2000-11-14
/ PRIOR APPLICATION NUMBER: US 60/249,570
/ PRIOR FILING DATE: 2000-11-16
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: PERL Program
/ SEQ ID NO 23
/ LENGTH: 1255
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. US20040053824A1 55022490CD1
US-10-312-352-23

Query Match 90.3%; Score 56; DB 15; Length 1255;
Best Local Similarity 66.7%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSKWSKCSXXCG 12
Db 113 WSKWSKCSXXCG 124

RESULT 9
US-10-225-567A-346
/ Sequence 23, Application US/10312352
/ Publication No. US20040053824A1
/ GENERAL INFORMATION:
/ APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
/ APPLICANT: YOE, Henry; AZIMZAI, Yalda
/ APPLICANT: HE, Ann; BATRA, Sajeev
/ APPLICANT: LO, Terence P.; NGUYEN, Danniell B.
/ APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
/ APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.
/ APPLICANT: LAL, Preeti G.; KEARNEY, Liam
/ APPLICANT: BURFORD, Neil; YAO, Monique G.
/ APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.
/ APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.
/ APPLICANT: BAUGHN, Mariah R.; HAPALIA, April, J.A.
/ APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
/ APPLICANT: LU, Yan; BOROWSKY, Mark L.
/ APPLICANT: LU, Dyrng Aina M.; RAMKUMAR, Jayalaxmi
/ APPLICANT: YANG, Junming; GURURAJAN, Rajagopal
/ APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.
/ APPLICANT: XU, Yuming; KALLICK, Deborah A.
/ APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha
/ APPLICANT: DELEGEANE, Angelo M.; LEE, Sally
/ TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
/ FILE REFERENCE: PF-0794 USN
/ CURRENT APPLICATION NUMBER: US/10/312,352
/ CURRENT FILING DATE: 2002-12-18
/ PRIOR APPLICATION NUMBER: PCT/US01/21067
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: US 60/215,454
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 60/219,462
/ PRIOR FILING DATE: 2000-07-
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US-10-386-414-2
; ORGANISM: Homo Sapien

Query Match 90.3%; Score 56; DB 15; Length 1686;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 4; Indels

Qy 1 WSXWSXCSXXCG 12
Db 544 WSAWSICSRSCG 555

RESULT 11

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US-09-788-043C-5
; Sequence 5, Application US/09788043C
; Patent No. US20020107361A1
; GENERAL INFORMATION:
; APPLICANT: Heller, Renu
; APPLICANT: Zuo, Fengrong
; APPLICANT: Klonowski, Paul
; TITLE OF INVENTION: No. US20020107361A1e1 Metalloproteases Having
; TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions
; FILE REFERENCE: ROCH-004
; CURRENT APPLICATION NUMBER: US/09/788,043C
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/184,152
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1690
; TYPE: PRT
; ORGANISM: human
US-09-788-043C-5

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Query Match 90.3%; Score 56; DB 9; Length 1690;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WSXWSXCSXXCG 12
Db 548 WSAWSICSRS CG 559

RESULT 12

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US-10-213-509-5
; Sequence 5, Application US/10213509
; Publication NO. US20030054485A1
; GENERAL INFORMATION:
; APPLICANT: Weiss, Joseph
; APPLICANT: Scott, Matthew
; TITLE OF INVENTION: JELLY BELLY GENES AND THEIR USES
; FILE REFERENCE: STAN-232
; CURRENT APPLICATION NUMBER: US/10/213,509
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/311,720
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4123
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-213-509-5

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Query Match      90.3%; Score 56; DB 14; Length 4123;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 WSXWSXCSXCG 12
Db 2518 WSVWSSCSRSG 252

RESULT 13

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US-10-085-198-2
; Sequence 2, Application US/10085198
; Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-2

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Query Match 90.3%; Score 56; DB 15; Length 4219;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WSXWSXCSXXCG 12
pb 2614 WSVWSSCSRS CG 2625

RESULT 14

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US-10-042-696-12
/ Sequence 12, Application US/10042696
/ Publication No. US20030171298A1
/ GENERAL INFORMATION:
/ APPLICANT: Tuszyński, George
/ APPLICANT: Williams, Taffy
/ APPLICANT: Actor, Paul
/ TITLE OF INVENTION: RETROINVERSO POLYPEPT
/ FILE REFERENCE: 07206-0021
/ CURRENT APPLICATION NUMBER: US/10/042,696
/ CURRENT FILING DATE: 2001-10-03
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: PatentIn Ver 2.0
/ SEQ ID NO 12
/ LENGTH: 23
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artifi
/ -OTHER INFORMATION: thrombospondin
US-10-042-696-12

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Query Match	88.7%	Score 55;	DB 14;	Length 23;
Best Local Similarity	66.7%	Pred. No. 0.73;		
Matches 8;	Conservative	0;	Mismatches 4;	Indels 0;
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Qy 1 WSXWSXCSXXCG 12
pb 4 WSPWSSCSVTG 15

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; SEQ ID NO 408
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-408

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Query Match 88.7%; Score 55; DB 15; Length 41;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 4; Indels

	Qy	1	WSXWSXC	SXXC	G	12
	D _b	3	WLSWSVC	SVTC	G	14

Search completed: April 1, 2005, 14:22:17
Job time : 63.8261 secs

RESULT 15

US-10-074-978A-408
; Sequence 408, Application US/10074978A
; Publication No. US20040010119A1

; PUBLICATION NO: 0520
; GENERAL INFORMATION:

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/ GENERAL INFORMATION:
/
/ APPLICANT: Leite, Mario
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Guo, Xiaojia (Sasha)
/ APPLICANT: Fernandes, Elma
/ APPLICANT: Li, Li
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Caaman, Stacie
/ APPLICANT: Boldos, Perenc
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Bialock, Angela
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Vernet, Corine
/ APPLICANT: Tchernev, Velizar T
/ APPLICANT: Malyankar, Uriel M
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Mezes, Peter S
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Heyes, Melvin P
/ APPLICANT: Herрман, John
/ APPLICANT: Pena, Carol E A
/ APPLICANT: Shimkets, Richard A
/ APPLICANT: Taupier Jr, Raymond J
/ APPLICANT: Moore, No. US20040010119A11le
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Edinger, Shlomit
/ APPLICANT: Gunther, Erik
/ APPLICANT: Stone, Dave
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Peyman, John
/ APPLICANT: Smithson, Glennnda
/ APPLICANT:
/
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUC
/
/ FILE REFERENCE: 21402-269

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; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 547
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; SOFTWARE: PatentIn Ver. 2.1
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:44:22 ; Search time 21.1304 Seconds
(without alignments)
42.393 Million cell updates/sec

Title: US-09-462-909D-7

Perfect score: 62

Sequence: 1 WSXWSXCSXXCG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	90.3	479	4	US-09-270-767-46823
2	56	90.3	677	4	US-09-270-767-58094
3	56	90.3	847	4	US-09-270-767-42783
4	56	90.3	997	3	US-09-369-364A-7
5	55	88.7	23	1	US-07-646-531D-6
6	55	88.7	23	2	US-08-488-273-6
7	55	88.7	23	3	US-09-197-770B-12
8	55	88.7	23	6	5426100-6
9	55	88.7	23	6	5426100-6
10	55	88.7	51	2	US-08-799-173A-11
11	55	88.7	51	4	US-09-170-042A-11
12	55	88.7	60	1	US-07-646-531D-12
13	55	88.7	60	2	US-08-488-273-12
14	55	88.7	60	6	5426100-12
15	55	88.7	60	6	5426100-12
16	55	88.7	218	3	US-08-985-526-1
17	55	88.7	239	5	PCT-US93-01652-1
18	55	88.7	441	3	US-08-985-526-3
19	55	88.7	568	1	US-07-862-021B-14
20	55	88.7	568	5	PCT-US93-03164-14
21	55	88.7	787	4	US-09-825-294-207
22	55	88.7	787	4	US-09-970-966-207
23	55	88.7	788	2	US-08-918-914-4
24	55	88.7	802	1	US-07-862-021B-12
25	55	88.7	802	1	US-08-313-288B-12
26	55	88.7	802	5	PCT-US93-03164-12
27	55	88.7	807	1	US-07-862-021B-10

28	55	88.7	807	1	US-08-313-288B-10	Sequence 10, Appl
29	55	88.7	807	4	US-09-132-769-1	Sequence 1, Appli
30	55	88.7	807	4	US-09-132-769-3	Sequence 3, Appli
31	55	88.7	807	4	US-09-132-769-5	Sequence 5, Appli
32	55	88.7	807	4	US-09-640-173-186	Sequence 186, App
33	55	88.7	807	4	US-09-713-550-186	Sequence 186, App
34	55	88.7	807	4	US-09-825-294-186	Sequence 186, App
35	55	88.7	807	4	US-09-970-966-186	Sequence 186, App
36	55	88.7	807	5	PCT-US93-03164-10	Sequence 10, Appl
37	55	88.7	1045	4	US-09-949-016-11112	Sequence 11112, A
38	55	88.7	1170	1	US-08-313-288B-20	Sequence 20, Appl
39	55	88.7	1170	4	US-09-657-472-2	Sequence 2, Appli
40	55	88.7	1172	1	US-08-313-288B-19	Sequence 19, Appl
41	55	88.7	1172	4	US-09-949-016-6333	Sequence 6333, Ap
42	55	88.7	1184	2	US-08-918-914-1	Sequence 1, Appli
43	55	88.7	1184	3	US-08-996-083-3	Sequence 3, Appli
44	55	88.7	1224	4	US-09-930-872-4	Sequence 10, Appli
45	55	88.7	1224	4	US-10-217-774-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-270-767-46823
; Sequence 46823, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46823
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46823

Query Match 90.3%; Score 56; DB 4; Length 479;
Best Local Similarity 66.7%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	1	WSXWSXCSXXCG	12
Db	242	WSEWSACSVC	253

RESULT 2

US-09-270-767-58094
; Sequence 58094, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58094
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-58094

Query Match 90.3%; Score 56; DB 4; Length 677;
Best Local Similarity 66.7%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	1	WSXWSXCSXXCG	12
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Db 434 WSWSDCSCSKCG 445

RESULT 3

US-09-270-767-42783

; Sequence 42783, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 42783

; LENGTH: 847

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-42783

Query Match 90.3%; Score 56; DB 4; Length 847;

Best Local Similarity 66.7%; Pred. No. 3.3;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSWXSCSXKCG 12

Db 434 WSWSDCSCSKCG 445

RESULT 4

US-09-369-364A-7

; Sequence 7, Application US/09369364A

; Patent No. 6391610

; GENERAL INFORMATION:

; APPLICANT: Apte, Suneel

; APPLICANT: Hurskainen, Tiina L.

; APPLICANT: Hirohata, Satoshi

; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases

; FILE REFERENCE: 26473/4007/10-30-00

; CURRENT APPLICATION NUMBER: US/09/369,364A

; CURRENT FILING DATE: 1999-08-06

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 997

; TYPE: PRT

; ORGANISM: Homo sapiens ADAMTS-7

US-09-369-364A-7

Query Match 90.3%; Score 56; DB 3; Length 997;

Best Local Similarity 66.7%; Pred. No. 3.8;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSWXSCSXKCG 12

Db 544 WSAWSICSRSCG 555

RESULT 5

US-07-646-531D-6

; Sequence 6, Application US/07646531D

; Patent No. 5200397

; GENERAL INFORMATION:

; APPLICANT: Deutch, Alan Howard

; APPLICANT: Tuszyński, George Paul

; TITLE OF INVENTION: Peptide Fragments and Analogs of

; TITLE OF INVENTION: Thrombospondin

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: W. R. Grace & Co.-Conn.

; STREET: 7379 Route 32

US-07-646-531D-6

Query Match 88.7%; Score 55; DB 1; Length 23;

Best Local Similarity 66.7%; Pred. No. 0.24;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSWXSCSXKCG 12

Db 4 WSPWSSCSVTCG 15

RESULT 6

US-08-488-273-6

; Sequence 6, Application US/08488273

; Patent No. 5840692

; GENERAL INFORMATION:

; APPLICANT: Deutch, Alan H.

; APPLICANT: Tuszyński, George P.

; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF

; TITLE OF INVENTION: THROMBOSPONDIN

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.

; STREET: 1601 Market Street, 36th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103-2398

; COMPUTER READABLE FORM: disk

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,273

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/359,263

; FILING DATE: 19-DEC-1994

; APPLICATION NUMBER: US 08/110,146

; FILING DATE: 20-AUG-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/896,527

; FILING DATE: 09-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/483,527

; FILING DATE: 22-FEB-1990

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; FILING DATE: 22-FEB-1990
; SEQ ID NO:6:
; LENGTH: 23
5426100-6

Query Match      88.7%; Score 55; DB 6; Length 23;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSWXKSCSXKCG 12
   |||||
DB 4 WSPWSSCSVTGC 15

RESULT 9
5426100-6
; Patent No. 5426100
; APPLICANT: DEUTCH, ALAN H.;TUSZYNSKI, GEORGE
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; . THROMBOSPONDIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 483,527
; FILING DATE: 22-FEB-1990
; SEQ ID NO:6:
; LENGTH: 23
5426100-6

Query Match      88.7%; Score 55; DB 6; Length 23;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSWXKSCSXKCG 12
   |||||
DB 4 WSPWSSCSVTGC 15

RESULT 10
US-08-799-173A-11
; Sequence 11, Application US/08799173A
; Patent No. 5871969
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG,
; APPLICANT: PATRICK J. DILLON
; TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,173A
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504

```

```
; NAME: Appleby, Vanessa L.
; REGISTRATION NUMBER: 33223
; REFERENCE/DOCKET NUMBER: 01-7896
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 531-4515
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-646-531D-12

Query Match      88.7%; Score 55; DB 1; Length 60;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 WSXWSXCSCXXCG 12
Db      7 WSPWSSCSVTCG 18

RESULT 13
US-08-488-273-12
; Sequence 12, Application US/08488273
; Patent No. 5840692
; GENERAL INFORMATION:
; APPLICANT: Deutch, Alan H.
; APPLICANT: Tuszyński, George P.
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; TITLE OF INVENTION: THROMBOSPONDIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,273
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/359,263
; FILING DATE: 19-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/896,527
; FILING DATE: 09-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/483,527
; FILING DATE: 22-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 567-2020
; TELEFAX: (215) 567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; STRANDEDNESS:

; NAME: Appleby, Vanessa L.
; REGISTRATION NUMBER: 33223
; REFERENCE/DOCKET NUMBER: 01-7896
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 531-4515
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-646-531D-12

Query Match      88.7%; Score 55; DB 2; Length 51;
Best Local Similarity 66.7%; Pred. No. 0.46;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 WSXWSXCSCXXCG 12
Db      6 WSEWSDCSVTCG 17

RESULT 11
US-09-170-042A-11
; Sequence 11, Application US/09170042A
; Patent No. 6759512
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg
; APPLICANT: Dillon, Patrick
; TITLE OF INVENTION: Human Neuronal Attachment Factor-1
; FILE REFERENCE: PF226D1
; CURRENT APPLICATION NUMBER: US/09/170,042A
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 11
; LENGTH: 51
; TYPE: PRT
; ORGANISM: rat
US-09-170-042A-11

Query Match      88.7%; Score 55; DB 4; Length 51;
Best Local Similarity 66.7%; Pred. No. 0.46;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 WSXWSXCSCXXCG 12
Db      6 WSEWSDCSVTCG 17

RESULT 12
US-07-646-531D-12
; Sequence 12, Application US/07646531D
; Patent No. 5200397
; GENERAL INFORMATION:
; APPLICANT: Deutch, Alan Howard
; APPLICANT: Tuszyński, George Paul
; TITLE OF INVENTION: Peptide Fragments and Analogs of
; TITLE OF INVENTION: Thrombospondin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. R. Grace & Co.-Comm.
; STREET: 7379 Route 32
; CITY: Columbia
; STATE: Maryland
; COUNTRY: USA
; ZIP: 21044
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/646,531D
; FILING DATE: 19910131
; ATTORNEY/AGENT INFORMATION:
```

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-273-12

Query Match 88.7%; Score 55; DB 2; Length 60;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 WSXWSXCSXXCG 12
DB 7 WSPWSSCSVTCTG 18

RESULT 14
5426100-12
; Patent No. 5426100
; APPLICANT: DEUTCH, ALAN H.; TUSZYNSKI, GEORGE
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; THROMBOSPONDIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 483,527
; FILING DATE: 22-FEB-1990
; SEQ ID NO: 12:
; LENGTH: 60
5426100-12

Query Match 88.7%; Score 55; DB 6; Length 60;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 WSXWSXCSXXCG 12
DB 7 WSPWSSCSVTCTG 18

RESULT 15
5426100-12
; Patent No. 5426100
; APPLICANT: DEUTCH, ALAN H.; TUSZYNSKI, GEORGE
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; THROMBOSPONDIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 483,527
; FILING DATE: 22-FEB-1990
; SEQ ID NO: 12:
; LENGTH: 60
5426100-12

Query Match 88.7%; Score 55; DB 6; Length 60;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 WSXWSXCSXXCG 12
DB 7 WSPWSSCSVTCTG 18

Search completed: April 1, 2005, 14:01:57
Job time : 22.1304 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 13:22:55 ; Search time 83.7391 Seconds
(without alignments)
55.424 Million cell updates/sec

Title: US-09-462-909D-7

Perfect score: 62

Sequence: 1 WSXWSXCSXXG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A Geneseq 16Dec04:*

1: Genesecp19808:*

2: Genesecp19908:*

3: Genesecp20008:*

4: Genesecp20018:*

5: Genesecp20028:*

6: Genesecp20038:*

7: Genesecp20038s:*

8: Genesecp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	91.9	324	8 ADP04871	Adp04871 Sea squirt
2	56	90.3	12	2 AA097445	Aa097445 Peptide t
3	56	90.3	27	4 AA04264	Aa04264 Human gen
4	56	90.3	100	4 AA04262	Aa04262 Human gen
5	56	90.3	149	4 AA04263	Aa04263 Human gen
6	56	90.3	189	4 AA04268	Aa04268 Human gen
7	56	90.3	191	4 AA04266	Aa04266 Human gen
8	56	90.3	206	3 AA08135	Aa08135 Amino aci
9	56	90.3	763	4 AB062815	Ab062815 Drosophil
10	56	90.3	997	4 AB072283	Ab072283 Human ADA
11	56	90.3	997	7 AD069288	Ad069288 Human hea
12	56	90.3	1083	4 AB061710	Ab061710 Drosophil
13	56	90.3	1255	5 AD128031	Ad128031 ECMCAD pr
14	56	90.3	1515	8 AD029008	Ad029008 Mouse nov
15	56	90.3	1522	2 AA099302	Aa099302 Human BAI
16	56	90.3	1522	3 AA023601	Aa023601 Human sec
17	56	90.3	1522	6 AB081930	Ab081930 Human bra
18	56	90.3	1522	8 AD029007	Ad029007 Human nov
19	56	90.3	1682	4 AB066442	Ab066442 Drosophil
20	56	90.3	1686	4 AA000934	Aa000934 Human 278
21	56	90.3	1686	4 AA000913	Aa000913 Human 278
22	56	90.3	1686	4 AA074944	Aa074944 Human ADA
23	56	90.3	1686	8 AD058902	Ad058902 Human ADA
24	56	90.3	1690	4 AA086949	Aa086949 Human met
25	56	90.3	1784	3 AA041379	Aa041379 Human ORF

ALIGNMENTS

RESULT 1

ADP04871
ID ADP04871 standard; protein; 324 AA.

XX AC ADP04871;

XX DT 29-JUL-2004 (first entry)

XX DE Sea squirt protein with tissue specific expression in development Seq466.
XX KW sea squirt; regeneration medicine; gene therapy; cell proliferation;
XX KW differentiation; reproduction; environmental measurement; water survey.

XX OS Ciona intestinalis.

XX PN JP2004057129-A.

XX PD 26-FEB-2004.

XX PF 31-JUL-2002; 2002JP-00222593.

XX PR 31-JUL-2002; 2002JP-00222593.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI: 2004-287079/27.

XX N-PSDB; ADP04870.

XX Novel gene cluster which is specifically expressed in tissue or organ during developmental phase of sea squirt, useful for elucidation of mechanism of development of tissue or organ of sea squirt.

XX Claim 1; SEQ ID NO 466; 1846bp; Japanese.

XX This invention relates to novel genes and the encoded proteins thereof that are derived from the sea squirt Ciona intestinalis. Specifically, it refers to those genes that are expressed in the tissues or organs of the sea squirt during its developmental phase. The present invention describes the identification of these genes as useful for elucidation of the mechanism of development and hence for developing regeneration medicines and gene therapy techniques. Accordingly, they can be used in the research of various genetic diseases, as well as the analysis of cell proliferation, differentiation and reproduction. Furthermore, such compositions can be useful for environmental measurements and water surveys, particularly for sea water surveys, and also for the preparation of transformed sea squirt for improving edibility of sea squirt such as Halocynthia roretzi. This polypeptide sequence is a sea squirt protein sequence that has tissue specific expression during development, given in

Abu62079 Human jel
Adh48718 NOVI prot
Abg30203 Novel hum
Adn95228 Human BEC
Abg21064 Novel hum
Aar13630 Thrombosop
Aar13630 Thrombosop
Aae20782 Alternati
Adm80538 Thrombosop
Add44504 Polypepti
Aaw92465 Rat F-spo
Adq94995 Rat F-spo
Adr03574 Rat F-spo
Aay49504 Human MET
Aay49507 Human MET
Aag79062 Biologica
Aag79061 Biologica
Aab50006 TSP1 doma
Aab50009 TSP2 doma
Aar13641 Thrombosop

Fri Apr 1 15:03:04 2005

CC an exemplification of the invention.
 XX
 SQ Sequence 324 AA;
 Query Match 91.9%; Score 57; DB 8; Length 324;
 Best Local Similarity 66.7%; Pred. No. 2.9;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WSXWSXCSXXCG 12
 Db 85 WSSWSRCSXSCG 96
 RESULT 2
 AAW97445
 ID AAW97445 standard; peptide; 12 AA.
 XX
 AC AAW97445;
 XX
 DT 19-MAY-1999 (first entry)
 XX
 DE Peptide that is useful for regenerating the nervous system.
 XX
 KW Neuronal sprouting; cerebral cortex; spinal cord cell; aggregation;
 KW neurite defasciculation; regeneration; nervous system cell;
 KW neurodegeneration; Alzheimer's; Parkinson's disease; multiple sclerosis;
 KW myopathy; synapse formation; neuroblastoma.
 XX
 OS Synthetic.
 XX
 WO9903890-A1.
 FN
 XX
 PD 28-JAN-1999.
 XX
 PF 16-JUL-1998; 98WO-FR001556.
 XX
 PR 16-JUL-1997; 97FR-00009016.
 XX
 PA (UYAU-) UNIV AUVERGNE.
 XX
 PI Meinel A, Monnerie H, Gobron S;
 XX
 DR WPI; 1999-132166/11.
 XX
 PT New polypeptides for promoting growth of neurons - useful for treatment
 of neurodegeneration, neuroblastoma and as additives for neuronal cell
 cultures.
 XX
 PS Claim 6; Page 14; 29pp; French.
 XX
 CC The present sequence represents a peptide that stimulates neuronal
 (particularly axonal) sprouting in neurons of the cerebral cortex, and in
 spinal cord cells inhibits aggregation and defasciculation of neurites
 while increasing formation of synaptic contacts. The peptide is used to
 regenerate nervous system cells, particularly for treating
 neurodegeneration (e.g. Alzheimer's or Parkinson's diseases, multiple
 sclerosis and myopathy), other conditions requiring regeneration
 (particularly elongation and synapse formation) or neuroblastoma. The
 peptide can also be used as an additive for neuronal cell cultures
 XX
 SQ Sequence 12 AA;
 Query Match 90.3%; Score 56; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 0.25;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WSXWSXCSXXCG 12
 Db 1 WSGWSSCSXSCG 12
 RESULT 3
 AAE04264

AAE04264 standard; peptide; 27 AA.
 AAE04264;
 09-AUG-2001 (first entry)
 Human gene 8 encoded secreted protein fragment, SEQ ID NO:127.
 Human; secreted protein; proliferative disorder; cancer; tumour;
 foetal abnormality; developmental abnormality; haematopoietic disorder;
 immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 inflammation; allergy; neurological disorder; Alzheimer's disease;
 Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 cardiovascular disorder; angiotensin disorder; kidney disorder;
 gastrointestinal disorder; pregnancy-related disorder; gene therapy;
 endocrine disorder; infection; wound healing; vulnery; cell culture;
 chemotaxis; food additive; binding partner identification; chromosome 7.
 Homo sapiens.
 WO200136432-A2.
 25-MAY-2001.
 15-NOV-2000; 2000WO-US031162.
 19-NOV-1999; 99US-0166415P.
 30-JUN-2000; 2000US-0215136P.
 (HUMA-) HUMAN GENOME SCI INC.
 Ruben SM, Komatsoulis GA, Baker KP, Young PE;
 WPI; 2001-343793/36.
 Isolated nucleic acid molecule encoding a human secreted protein is used
 in preventing, treating or ameliorating a medical condition.
 Disclosure; Page 32; 509pp; English.
 AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted
 protein genes, and AAE04199-AAE04239 represent the proteins they encode.
 AAE04240-AAE04297 represent human secreted protein fragments or variants.
 The secreted proteins and their genes are useful for preventing, treating
 or ameliorating medical conditions, e.g., by protein or gene therapy.
 Pathological conditions can be diagnosed by determining the amount of the
 new protein in a sample or by determining the presence of mutations in
 the new genes. Specific uses are described for each of the 18 genes,
 based on the tissues in which they are most highly expressed, and include
 developing products for the diagnosis or treatment of proliferative
 disorders, cancer, tumours, foetal and developmental abnormalities,
 haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 diseases (e.g., rheumatoid arthritis), inflammation, allergies, disease),
 neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 angiogenic disorders, kidney disorders, gastrointestinal disorders,
 pregnancy-related disorders, endocrine disorders, and infectious. The
 proteins can also be used to aid wound healing and epithelial cell
 proliferation, to prevent skin ageing due to sunburn, to maintain organs
 before transplantation, for supporting cell culture of primary tissues,
 to regenerate tissues, to identify their cognate ligands or binding
 partners, and in chemotaxis, and can be used as a food additive or
 preservative to modify storage properties. Antibodies specific for a
 protein of the invention can be used in alleviating symptoms associated
 with the disorders mentioned above, and in diagnostic immunoassays e.g.,
 radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
 present sequence represents a human secreted protein fragment referred to
 in the disclosure of the invention
 Sequence 27 AA;

Query Match 90.3%; Score 56; DB 4; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.5;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
DB 13 WSAWSSCSAPCG 24

RESULT 4
AAE04262
ID AAE04262 standard; protein; 100 AA.
XX AAE04262;
XX
DT 09-AUG-2001 (first entry)
DE Human gene 8 encoded secreted protein fragment, SEQ ID NO:124.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiotensin-related disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
KW endocrine disorder; infection; wound healing; vulnerability; cell culture;
KW chemotaxis; food additive; binding partner identification; chromosome 7.
XX
OS Homo sapiens.
XX
PI Ruben SM, Komatsoulis GA, Baker KP, Young PE;
PI WPI; 2001-343793/36.
XX
DR Isolated nucleic acid molecule encoding a human secreted protein is used
XX in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; Page 493; 509pp; English.
XX
CC AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted
CC protein genes, and AAE04199-AAE04239 represent the proteins they encode.
CC AAE04240-AAE04297 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 18 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiotensin-related disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin ageing due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC

CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
CC present sequence represents a human secreted protein fragment referred to
CC in the disclosure of the invention
XX
SQ Sequence 100 AA;
Query Match 90.3%; Score 56; DB 4; Length 100;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
DB 11 WSAWSSCSAPCG 22

RESULT 5
AAE04263
ID AAE04263 standard; protein; 149 AA.
XX AAE04263;
XX
DT 09-AUG-2001 (first entry)
DE Human gene 8 encoded secreted protein fragment, SEQ ID NO:126.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiotensin-related disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
KW endocrine disorder; infection; wound healing; vulnerability; cell culture;
KW chemotaxis; food additive; binding partner identification; chromosome 7.
XX
OS Homo sapiens.
XX
PI Ruben SM, Komatsoulis GA, Baker KP, Young PE;
PI WPI; 2001-343793/36.
XX
DR Isolated nucleic acid molecule encoding a human secreted protein is used
XX in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; Page 493; 509pp; English.
XX
CC AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted
CC protein genes, and AAE04199-AAE04239 represent the proteins they encode.
CC AAE04240-AAE04297 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 18 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiotensin-related disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin ageing due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC

XX PD 25-MAY-2001.

XX PF 15-NOV-2000; 2000WO-US031162.

XX PR 19-NOV-1999; 99US-0166415P.

XX PR 30-JUN-2000; 2000US-0215136P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Komatsoulis GA, Baker KP, Young PE;

XX WPI; 2001-343793/36.

PT Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

XX Disclosure; Page 33; 509pp; English.

XX AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiotensin-related disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infectious diseases. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention

XX SQ Sequence 149 AA;

Query Match 90.3%; Score 56; DB 4; Length 149;

Best Local Similarity 66.7%; Pred. No. 2.1;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 WSXWSXCSXXCG 12
||| ||| |||

DB 1 WSAWSSCSAPCG 12
||| ||| |||

RESULT 6

AAE04268

ID AAE04268 standard; protein; 189 AA.

XX AC AAE04268;

XX DT 09-AUG-2001 (first entry)

XX DE Human gene 8 encoded secreted protein fragment, SEQ ID NO:131.

XX KW Human; secreted protein; proliferative disorder; cancer; tumour;

KW foetal abnormality; developmental abnormality; haematopoietic disorder;

KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;

KW inflammation; allergy; neurological disorder; Alzheimer's disease;

KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;

KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;

KW cardiovascular disorder; angiogenic disorder; kidney disorder;

KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;

KW endocrine disorder; infection; wound healing; vulvarity; cell culture;

KW chemotaxis; food additive; binding partner identification; chromosome 7.

XX OS Homo sapiens.

XX WO200136432-A2.

XX PN

XX PD 25-MAY-2001.

XX PF 15-NOV-2000; 2000WO-US031162.

XX PR 19-NOV-1999; 99US-0166415P.

XX PR 30-JUN-2000; 2000US-0215136P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Komatsoulis GA, Baker KP, Young PE;

XX WPI; 2001-343793/36.

PT Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

XX Disclosure; Page 33; 509pp; English.

XX AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiotensin-related disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infectious diseases. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention

XX SQ Sequence 149 AA;

Query Match 90.3%; Score 56; DB 4; Length 149;

Best Local Similarity 66.7%; Pred. No. 2.1;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 WSXWSXCSXXCG 12
||| ||| |||

DB 1 WSAWSSCSAPCG 12
||| ||| |||

RESULT 6

AAE04268

ID AAE04268 standard; protein; 189 AA.

XX AC AAE04268;

XX DT 09-AUG-2001 (first entry)

XX DE Human gene 8 encoded secreted protein fragment, SEQ ID NO:131.

XX KW Human; secreted protein; proliferative disorder; cancer; tumour;

KW foetal abnormality; developmental abnormality; haematopoietic disorder;

KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;

KW inflammation; allergy; neurological disorder; Alzheimer's disease;

KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;

KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;

KW cardiovascular disorder; angiogenic disorder; kidney disorder;

KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;

KW endocrine disorder; infection; wound healing; vulvarity; cell culture;

KW chemotaxis; food additive; binding partner identification; chromosome 7.

XX OS Homo sapiens.

XX WO200136432-A2.

XX PN

XX PD 25-MAY-2001.

XX PF 15-NOV-2000; 2000WO-US031162.

XX PR 19-NOV-1999; 99US-0166415P.

XX PR 30-JUN-2000; 2000US-0215136P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Komatsoulis GA, Baker KP, Young PE;

XX WPI; 2001-343793/36.

PT Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

XX Disclosure; Page 33; 509pp; English.

XX AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiotensin-related disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infectious diseases. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention

XX SQ Sequence 189 AA;

Query Match 90.3%; Score 56; DB 4; Length 189;

Best Local Similarity 66.7%; Pred. No. 2.5;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 WSXWSXCSXXCG 12
||| ||| |||

DB 1 WSAWSSCSAPCG 22
||| ||| |||

RESULT 7

AAE04266

ID AAE04266 standard; protein; 191 AA.

XX AC AAE04266;

XX DT 09-AUG-2001 (first entry)

XX DE Human gene 8 encoded secreted protein fragment, SEQ ID NO:129.

XX KW Human; secreted protein; proliferative disorder; cancer; tumour;

KW foetal abnormality; developmental abnormality; haematopoietic disorder;

KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;

KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiodysplasia; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
 KW endocrine disorder; infection; wound healing; vulnerability; cell culture;
 KW chemotaxis; food additive; binding partner identification; chromosome 7.
 XX
 OS Homo sapiens.
 XX
 XX WO200136432-A2.
 XX
 XX 25-MAY-2001.
 XX
 XX 15-NOV-2000; 2000WO-US031162.
 XX
 XX 19-NOV-1999; 99US-0166415P.
 XX 30-JUN-2000; 2000US-0215136P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Komatsoulis GA, Baker KP, Young PE;
 XX WPI; 2001-343793/36.
 XX
 DR Isolated nucleic acid molecule encoding a human secreted protein is used
 PT in preventing, treating or ameliorating a medical condition.
 XX
 XX Disclosure; Page 32; 509pp; English.

XX AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted
 CC protein genes, and AAE04199-AAE04239 represent the proteins they encode.
 CC AAE04240-AAE04297 represent human secreted protein fragments or variants.
 CC The secreted proteins and their genes are useful for preventing, treating
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.
 CC Pathological conditions can be diagnosed by determining the amount of the
 CC new protein in a sample or by determining the presence of mutations in
 CC the new genes. Specific uses are described for each of the 18 genes,
 CC based on the tissues in which they are most highly expressed, and include
 CC developing products for the diagnosis or treatment of proliferative
 CC disorders, cancer, tumours, foetal and developmental abnormalities,
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
 CC pregnancy-related disorders, endocrine disorders, and infections. The
 CC proteins can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin ageing due to sunburn, to maintain organs
 CC before transplantation; for supporting cell culture of primary tissues,
 CC to regenerate tissues, to identify their cognate ligands or binding
 CC partners, and in chemotaxis, and can be used as a food additive or
 CC preservative to modify storage properties. Antibodies specific for a
 CC protein of the invention can be used in alleviating symptoms associated
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
 CC present sequence represents a human secreted protein fragment referred to
 CC in the disclosure of the invention
 XX
 XX Sequence 191 AA;

Query Match 90.3%; Score 56; DB 4; Length 191;
 Best Local Similarity 66.7%; Pred. No. 2.5;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WSXWSXCSXXCG 12
 |||||
 DB 13 WSAWSSCSAPCG 24
 RESULT 8
 AAB08135

ID AAB08135 standard; protein; 206 AA.
 XX
 AC AAB08135;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Amino acid sequence of a KIAA0550 polypeptide.
 XX
 KW Type 1 repeat; thrombospondin-1; TSP-1; Type I repeat peptide; TRP;
 KW KIAA0688; KIAA0550; angiogenesis inhibitory protein; angiogenesis;
 KW cancer; tumour; rheumatoid arthritis; psoriasis; retinopathy;
 KW ocular angiogenic disease; macular degeneration; corneal graft rejection;
 KW neovascular glaucoma; retrolental fibroplasia; rubeosis;
 KW Osler-Webber Syndrome; myocardial angiogenesis; haemophilic joint;
 KW plaque neovascularisation; telangiectasia; angiofibroma;
 KW wound granulation; coronary collateral; cerebral collateral;
 KW arteriovenous malformation; ischemic limb angiogenesis;
 KW neovascular glaucoma; retrolental fibroplasia; fracture; vasculogenesis;
 KW heliobacter related disease; hematopoiesis; ovulation; menstruation;
 KW placental; birth control; embryo implantation.
 XX
 OS Homo sapiens.
 XX
 XX WO200047622-A2.
 XX
 XX 17-AUG-2000.
 XX
 XX 15-FEB-2000; 2000WO-GB000520.
 XX
 XX 15-FEB-1999; 99GB-00003408.
 XX
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 XX Mazarakis N, Martin-Rendon E, Kingsman SM;
 XX WPI; 2000-549137/50.
 XX
 XX Non-naturally occurring Type I repeat peptide (TRP) derived from human
 PT thrombospondin-1, KIAA0688 or KIAA0550 proteins, useful in the treatment
 PT of angiogenesis and/or cancer.
 XX
 XX Claim 5; Fig 7; 84pp; English.

The present sequence represents a KIAA0550 polypeptide. The specification
 CC describes a non-naturally occurring Type I repeat peptide (TRP) derived
 CC from human thrombospondin-1 (hrsp-1), KIAA0688 or KIAA0550 proteins. The
 CC TRP protein is an angiogenesis inhibitory protein. TRP proteins are used
 CC for the treatment of conditions associated with angiogenesis and cancer.
 CC Angiogenic mediated diseases include tumours, rheumatoid arthritis,
 CC psoriasis, ocular angiogenic diseases, retinopathy of prematurity,
 CC macular degeneration, corneal graft rejection, neovascular glaucoma,
 CC retrolental fibroplasia, rubeosis), Osler-Webber Syndrome, myocardial
 CC angiogenesis, plaque neovascularisation, telangiectasia, haemophilic
 CC joints, angiofibroma, wound granulation, coronary collaterals, cerebral
 CC collaterals, arteriovenous malformations, ischemic limb angiogenesis,
 CC neovascular glaucoma, retrolental fibroplasia, heliobacter related
 CC diseases, fractures, vasculogenesis, hematopoiesis, ovulation,
 CC menstruation and placental. TRPs are also useful in the treatment of
 CC disease of excessive or abnormal stimulation of endothelial cells. TRP
 CC can also be used as a birth control agent, as it prevents the
 CC vascularisation required for embryo implantation
 XX
 XX Sequence 206 AA;

Query Match 90.3%; Score 56; DB 3; Length 206;
 Best Local Similarity 66.7%; Pred. No. 2.7;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WSXWSXCSXXCG 12
 |||||
 DB 5 WSAWSSCSVTCG 16

OS Homo sapiens.

XX PN WO2003087768-A2.
 XX PR 23-OCT-2003.
 XX PD
 XX PF 04-APR-2003; 2003WO-US010870.
 XX PR 12-APR-2002; 2002US-0372843P.
 XX PR 17-JUN-2002; 2002US-0389987P.
 XX PR 20-SEP-2002; 2002US-0412418P.
 XX PA (MITO-) MITOKOR.
 XX PA (BUCK-) BUCK INST AGE RES.
 XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 XX PI Warnock DE;
 XX DR WPI; 2003-845369/78.
 XX PR Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function.
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX PR Claim 1; SEQ ID NO 1094; 180pp; English.
 XX CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, neurotropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytosstatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX SQ Sequence 997 AA;
 Query Match 90.3%; Score 56; DB 7; Length 997;
 Best Local Similarity 66.7%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WSXWSXCSXXCG 12
 DB 544 WSAWSICRSRSG 555
 RESULT 12
 ID ABB61710 standard; protein; 1083 AA.
 AC ABB61710;
 XX 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 11922.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 XX 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX PI WPI; 2001-656860/75.
 XX DR N-PSDB; ABL05813.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX PS Disclosure; SEQ ID NO 11922; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 1083 AA;
 Query Match 90.3%; Score 56; DB 4; Length 1083;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WSXWSXCSXXCG 12
 DB 846 WSEWSACSVTCG 857
 RESULT 13
 ID ADI28031 standard; protein; 1255 AA.
 XX ADI28031;
 XX 15-APR-2004 (first entry)
 DE ECMCAD protein 55022490CD1.
 KW neurotropic; antitickling; antianemic; antitumor; anti-HIV; antiallergic;
 KW antianemic; antisthmatic; immunosuppressive; antithrombotic; antidiabetic;
 KW dermatological; nephrotrophic; antitumor; antithyroid; neuroprotective;
 KW osteopathic; antipsoriatic; antirheumatic; antithyroid; antitumor;
 KW antinflammatory; ophthalmological; anticonvulsant; antiparkinsonian;
 KW antibacterial; virucide; tranquilizer; neuroleptic; antidiabetic;
 KW cytosstatic; hepatotropic; gene therapy;
 KW human extracellular matrix and cell adhesion molecule; ECMCAD; diagnosis;
 KW genetic disorder; adrenoleukodystrophy; Down's syndrome; cystic fibrosis;
 KW Gaucher's disease; myotonic dystrophy; sickle cell anemia; thalassemia;
 KW Wilms' tumor; immunological disorder; acquired immunodeficiency syndrome;
 KW AIDS; adult respiratory distress syndrome; allergy; anemia; asthma;
 KW atherosclerosis; autoimmune hemolytic anemia; contact dermatitis;
 KW Goodpasture's syndrome; gout; Grave's disease; multiple sclerosis;
 KW osteoporosis; psoriasis; rheumatoid arthritis; scleroderma;
 KW systemic lupus erythematosus; ulcerative colitis; uveitis;
 KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; multiple sclerosis;
 KW meningitis; periodic paralysis; mental disorder; mood; anxiety;
 KW schizophrenia; amnesia; diabetic neuropathy; connective tissue disorder;
 KW osteoporosis; Paget's disease; osteonecrosis; osteomyelitis;
 KW chondrosarcoma; giant cell tumor; psoriatic arthritis;
 KW infectious arthritis; systemic sclerosis; cell proliferative disorder;
 KW actinic keratosis; atherosclerosis; hepatitis; psoriasis; cancer;

adenocarcinoma; leukemia; lymphoma; melanoma; myeloma.
 Homo sapiens.
 WO200202634-A2.
 10-JAN-2002.
 29-JUN-2001; 2001WO-US021067.
 30-JUN-2000; 2000US-0215454P.
 18-JUL-2000; 2000US-0219462P.
 12-OCT-2000; 2000US-0240106P.
 12-OCT-2000; 2000US-0240111P.
 27-OCT-2000; 2000US-0244021P.
 14-NOV-2000; 2000US-0248887P.
 16-NOV-2000; 2000US-0249570P.
 (INCY-) INCYTE GENOMICS INC.
 Tang YT, Yue H, Azinzai Y, He A, Batra S, Lo TP, Nguyen DB;
 Burdill JD, Marcus GA, Zingler KA, Gandhi AR, Lal P, Kearney L;
 Burford N, Yao MG, Walla NK, Elliot VS, Patterson C, Khan FA;
 Baughn WR, Hafalia AJA, Policky JL, Au-Young J, Lu Y, Borowsky ML;
 Lu DAM, Ramkumar J, Yang J, Gururajan R, Warren BA, Gietzen K;
 Xu Y, Kallick DA, Lee EA, Thangavelu K, Delegeane AM, Lee S;
 WPI; 2002-154732/20.
 N-PSDB; ADI28067.
 Novel isolated human extracellular matrix and cell adhesion molecules
 useful for treating, preventing connective tissue disorder e.g.
 osteoporosis, Paget's disease, genetic disorder e.g. cystic fibrosis,
 PT thalassemia.
 Claim 1; SEQ ID NO 23; 270pp; English.
 The invention relates to a novel isolated human extracellular matrix and
 cell adhesion molecule (referred to as ECMAD 1-36), its biologically
 active or immunogenic fragment or a sequence comprising 90 % identity to
 ECMAD 1-36. The molecule is useful for screening a compound for
 effectiveness as agonist or antagonist of itself. The protein and its
 encoding nucleic acid are useful in the diagnosis, treatment and
 prevention of genetic disorder such as adrenoleukodystrophy, Down's
 syndrome, cystic fibrosis, Gaucher's disease, myotonic dystrophy, sickle
 cell anemia, thalassemia, Wilms' tumor, etc., immunological disorders such
 as acquired immunodeficiency syndrome (AIDS), adult respiratory distress
 syndrome, allergies, anemia, asthma, atherosclerosis, autoimmune
 hemolytic anemia, contact dermatitis, Goodpasture's syndrome, gout,
 Grave's disease, multiple sclerosis, osteoporosis, psoriasis, rheumatoid
 arthritis, scleroderma, systemic lupus erythematosus, ulcerative colitis,
 arthritis, etc., a neurological disorder such as epilepsy, stroke,
 Alzheimer's disease, Huntington's disease, Parkinson's disease, multiple
 sclerosis, bacterial and viral meningitis, periodic paralysis, mental
 disorders including mood, anxiety, and schizophrenic disorders, amnesia,
 diabetic neuropathy, etc., connective tissue disorder such as
 osteoporosis, Paget's disease, osteonecrosis, osteomyelitis,
 chondrosarcoma, giant cell tumor, psoriatic arthritis, infectious
 arthritis, systemic sclerosis, etc., and a cell proliferative disorder
 such as actinic keratosis, atherosclerosis, hepatitis, psoriasis, cancers
 including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, etc.
 This sequence represents one of the novel proteins.

Sequence 1255 AA;

Query Match 90.3%; Score 56; DB 5; Length 1255;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WSWXSCSXCG 12
 Db 113 WSAWICSRCG 124

RESULT 14
 ADO29008
 ID ADO29008 standard; protein; 1515 AA.
 XX
 AC ADO29008;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Mouse novel GPCR BAI3, SEQ ID NO:107.
 XX
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 transgenic mouse; neurological disorder; adrenal gland disorder;
 colon disorder; intestinal disorder; cardiovascular disorder;
 muscular disorder; blood disorder; immune disorder; bone disorder;
 joint disorder; metabolic disorder; nutritive disorder; cancer;
 kidney disorder; liver disorder; lung disorder; breast disorder;
 ovary disorder; uterus disorder; prostate disorder; spleen disorder;
 skin disorder; stomach disorder; pancreas disorder; antidiabetic;
 thymus disorder; thyroid disorder; antiparkinsonian; antitumor;
 cytostatic; antiinflammatory; vasotropic; antiangiogenic; antidiabetic;
 CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
 dermatological; antiulcer; antithyroid; antiallergic; anorectic;
 immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
 murine; receptor.
 XX
 OS Mus musculus.
 XX
 PN WO2004040000-A2.
 XX
 PD 13-MAY-2004.
 XX
 PF 09-SEP-2003; 2003WO-US028226.
 XX
 PR 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX
 PA (PRIM-) PRIMAL INC.
 XX
 PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 WPI; 2004-390329/36.
 DR N-PSDB; ADO29009.
 XX
 PT Novel mammalian G protein coupled receptors, useful for identifying
 compounds that modulates diagnosing and treating disease condition
 associated with GPCR dysfunction e.g. autoimmune diseases, angina
 pectoris, Parkinson's disease.
 XX
 PS Claim 1; SEQ ID NO 107; 542pp; English.
 XX
 CC The invention relates to human and mouse G protein-coupled receptors
 (GPCRs) and nucleic acids encoding them. The invention also relates to
 sequences at least 90% identical to the GPCR proteins and nucleic acids
 of the invention; methods of treating, preventing or diagnosing diseases
 associated with GPCRs of the invention; methods of screening for
 compounds useful in the treatment of GPCR-related diseases; a transgenic
 mouse comprising a GPCR gene of the invention; a mouse comprising a
 mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 from the transgenic mice; kits comprising several mice, each of which has
 a mutation in a different GPCR gene of the invention; and kits comprising
 probes which hybridise to GPCR polynucleotides of the invention. The
 invention further discloses variants of the GPCR polypeptides and vectors
 comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 be used in the diagnosis, treatment or prevention of a wide variety of
 diseases including neurological disorders (e.g., Alzheimer's disease,
 depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 disorders of the adrenal gland; disorders of the colon or intestine
 (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 myocardial infarction); muscular disorders; blood disorders (e.g.,

CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX

SQ Sequence 1515 AA;

Query Match 90.3%; Score 56; DB 8; Length 1515;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
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 Db 297 WSQWSACSVCVG 308

RESULT 15

AAW99302
 ID AAW99302 standard; protein; 1522 AA.

AC AAW99302;

DT 21-MAY-1999 (first entry)

DE Human BAI3 protein.

KW Human; BAI3; brain; cancer; drug; diagnosis; prevention; treatment.

OS Homo sapiens.

PN JP11032766-A.

PD 09-FEB-1999.

PF 16-JUN-1997; 97JP-00176485.

PR 23-MAY-1997; 97JP-00150460.

XX (SAKA) OTSUKA PHARM CO LTD.

DR WPI; 1999-183823/16.

DR N-PSDB; AAX21357.

PT New human BAI gene - is expressed in brain plays important role in cancer
 PT formation.

PS Claim 2; Page 26-30; 62pp; Japanese.

XX This sequence represents the human BAI3 protein. The gene is expressed
 CC specifically in the brain and plays an important role in cancer formation
 CC in the brain. The BAI3 protein can be used in drug compositions to
 CC diagnose, prevent or treat such cancers
 XX

SQ Sequence 1522 AA;

Query Match 90.3%; Score 56; DB 2; Length 1522;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
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 Db 297 WSQWSACSVCVG 308

Search completed: April 1, 2005, 13:54:24
 Job time : 86.7391 secs

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